

# Sequence Listing

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 Eaton, Dan L.  
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 Gao, Wei-Qiang  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, Christopher J.  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Pan, James  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Smith, Victoria  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Watanabe, Colin K.  
 Williams, P. Mickey  
 Wood, William I.

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<223> Signal Peptide  
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<221> misc\_feature

<222> 36-47, 108-113, 166-171,198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature  
<222> 39-42  
<223> Glycosaminoglycan Attachment Site.

<220>  
<221> TRANSMEM  
<222> 136-152  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 161-163, 187-190 and 253-256  
<223> N-glycosylation Sites.

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Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys  
20 25 30  
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45  
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60  
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75  
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90  
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105  
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120  
Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu  
125 130 135  
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro  
140 145 150  
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val  
155 160 165  
Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys  
170 175 180  
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys  
185 190 195



Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys  
200 205 210

Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala  
215 220 225

Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu  
230 235 240

Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser  
245 250 255

Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His  
260 265 270

Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys  
275 280 285

Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala  
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Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn  
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Pro Lys Ala Val ..

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<212> DNA  
<213> Homo sapiens

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aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050  
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cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
gtctcacagg ggataagaag ttccaggagg cagtggagaa ggtgacacag 1300  
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<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

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 20 25 30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro  
 35 40 45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
 50 55 60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
 65 70 75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
 80 85 90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys
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Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val
				125					130					135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro
				140					145					150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro
				155					160					165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly
				170					175					180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro
				185					190					195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly
				200					205					210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg
				215					220					225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln
				230					235					240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp
				245					250					255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly
				260					265					270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe
				275					280					285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile
				290					295					300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser
				305					310					315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu
				320					325					330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu
				335					340					345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn
				350					355					360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser
				365					370					375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr
				380					385					390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe

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Arg	Glu	Leu	Ser	Arg 410	Leu	Thr	Gly	Asp	Lys 415	Lys	Phe	Gln	Glu	Ala 420	
Val	Glu	Lys	Val	Thr 425	Gln	His	Ile	His	Gly 430	Leu	Ser	Gly	Lys	Lys 435	
Asp	Gly	Leu	Val	Pro 440	Met	Phe	Ile	Asn	Thr 445	His	Ser	Gly	Leu	Phe 450	
Thr	His	Leu	Gly	Val 455	Phe	Thr	Leu	Gly	Ala 460	Arg	Ala	Asp	Ser	Tyr 465	
Tyr	Glu	Tyr	Leu	Leu 470	Lys	Gln	Trp	Ile	Gln 475	Gly	Gly	Lys	Gln	Glu 480	
Thr	Gln	Leu	Leu	Glu 485	Asp	Tyr	Val	Glu	Ala 490	Ile	Glu	Gly	Val	Arg 495	
Thr	His	Leu	Leu	Arg 500	His	Ser	Glu	Pro	Ser 505	Lys	Leu	Thr	Phe	Val 510	
Gly	Glu	Leu	Ala	His 515	Gly	Arg	Phe	Ser	Ala 520	Lys	Met	Asp	His	Leu 525	
Val	Cys	Phe	Leu	Pro 530	Gly	Thr	Leu	Ala	Leu 535	Gly	Val	Tyr	His	Gly 540	
Leu	Pro	Ala	Ser	His 545	Met	Glu	Leu	Ala	Gln 550	Glu	Leu	Met	Glu	Thr 555	
Cys	Tyr	Gln	Met	Asn 560	Arg	Gln	Met	Glu	Thr 565	Gly	Leu	Ser	Pro	Glu 570	
Ile	Val	His	Phe	Asn 575	Leu	Tyr	Pro	Gln	Pro 580	Gly	Arg	Arg	Asp	Val 585	
Glu	Val	Lys	Pro	Ala 590	Asp	Arg	His	Asn	Leu 595	Leu	Arg	Pro	Glu	Thr 600	
Val	Glu	Ser	Leu	Phe 605	Tyr	Leu	Tyr	Arg	Val 610	Thr	Gly	Asp	Arg	Lys 615	
Tyr	Gln	Asp	Trp	Gly 620	Trp	Glu	Ile	Leu	Gln 625	Ser	Phe	Ser	Arg	Phe 630	
Thr	Arg	Val	Pro	Ser 635	Gly	Gly	Tyr	Ser	Ser 640	Ile	Asn	Asn	Val	Gln 645	
Asp	Pro	Gln	Lys	Pro 650	Glu	Pro	Arg	Asp	Lys 655	Met	Glu	Ser	Phe	Phe 660	
Leu	Gly	Glu	Thr	Leu 665	Lys	Tyr	Leu	Phe	Leu 670	Leu	Phe	Ser	Asp	Asp 675	
Pro	Asn	Leu	Leu	Ser 680	Leu	Asp	Ala	Tyr	Val 685	Phe	Asn	Thr	Glu	Ala 690	

His Pro Leu Pro Ile Trp Thr Pro Ala  
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<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
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<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
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<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-44  
<223> Synthetic construct.

<400> 15  
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<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
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gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150  
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgttg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

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cgggcagtca ggggacaagg gcaggagacc tcggggccctc cccgtgcctg 300
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<210> 17
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<212> PRT
<213> Homo sapiens
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<221> sig_peptide
<222> 1-42
<223> Signal peptide.

<220>
<221> misc_feature
<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

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          20             25             30
Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
          35             40             45
Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
          50             55             60
Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
          65             70             75
Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
          80             85             90
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
          95             100             105
Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
          110             115             120
Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
          125             130             135
His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

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				140					145					150
Glu	Ser	Ser	Asn	Ser 155	Thr	Asp	Tyr	Ile	Ala 160	Met	His	Asp	Val	Asp 165
Leu	Leu	Pro	Leu	Asn 170	Glu	Glu	Leu	Asp	Tyr 175	Gly	Phe	Pro	Glu	Ala 180
Gly	Pro	Phe	His	Val 185	Ala	Ser	Pro	Glu	Leu 190	His	Pro	Leu	Tyr	His 195
Tyr	Lys	Thr	Tyr	Val 200	Gly	Gly	Ile	Leu	Leu 205	Leu	Ser	Lys	Gln	His 210
Tyr	Arg	Leu	Cys	Asn 215	Gly	Met	Ser	Asn	Arg 220	Phe	Trp	Gly	Trp	Gly 225
Arg	Glu	Asp	Asp	Glu 230	Phe	Tyr	Arg	Arg	Ile 235	Lys	Gly	Ala	Gly	Leu 240
Gln	Leu	Phe	Arg	Pro 245	Ser	Gly	Ile	Thr	Thr 250	Gly	Tyr	Lys	Thr	Phe 255
Arg	His	Leu	His	Asp 260	Pro	Ala	Trp	Arg	Lys 265	Arg	Asp	Gln	Lys	Arg 270
Ile	Ala	Ala	Gln	Lys 275	Gln	Glu	Gln	Phe	Lys 280	Val	Asp	Arg	Glu	Gly 285
Gly	Leu	Asn	Thr	Val 290	Lys	Tyr	His	Val	Ala 295	Ser	Arg	Thr	Ala	Leu 300
Ser	Val	Gly	Gly	Ala 305	Pro	Cys	Thr	Val	Leu 310	Asn	Ile	Met	Leu	Asp 315
Cys	Asp	Lys	Thr	Ala 320	Thr	Pro	Trp	Cys	Thr 325	Phe	Ser			

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<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.
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<210> 19
<211> 24
<212> DNA
<213> Artificial
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27

<222> 1-24  
<223> Synthetic construct

<400> 19  
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<210> 20  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 20  
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<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
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gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagatagggg acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser	Ser												
				20				25					30													
Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Pro	Ser												
				35				40					45													
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<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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 <212> PRT  
 <213> Homo sapiens

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 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
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 <223> Transmembrane domain (type II).

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 35 40 45  
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 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
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 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
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Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val					
				410					415					420					
Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr					
				425					430					435					
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu					
				440					445					450					
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu					
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Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys					
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Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu					
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Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala					
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg					
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Gln	Leu	Ser	Phe	Lys	Cys	Asn	Val	Ser	Asn	Thr	Phe	Ser	Ser	Leu					
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<223> Synthetic construct

<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

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<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

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<213> Homo sapiens

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<210> 31  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
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 50 55 60  
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 65 70 75  
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
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 155 160 165  
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
 170 175 180  
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
 185 190 195  
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 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu  
215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu  
245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln  
260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr  
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Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr  
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<210> 32  
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<212> DNA  
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taatataaaaa atcttttataa atcttctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120
Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro  
245 250 255  
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala  
260 265 270  
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser  
275 280 285  
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu  
290 295 300  
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser  
305 310 315  
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala  
320 325 330  
Glu Pro Glu Glu Gln  
335

<210> 34  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct

<400> 34  
tgctctttgt cccagacttc tgtcc 25

<210> 35  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 35  
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

<210> 36  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 36





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gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaacttc aaggcgagtc attcccctcc tttgaatcta 550  
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650  
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgcccat ctgagcacat cccaatgcta cacctgctct 750  
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800  
ctgataacag ttccattaca gtttagcatcc tctcttcaga accaacttct 850  
ccatctgtga ccccttgat agtggaacca agtggatggc ttaccacaaa 900  
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catagcccag agttttctggtt attgggaaat tgaggcaata gaaatgacag 1850  
acctgtattc tagtacgtta taatttttcta gatcagcaca cacatgatca 1900  
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000  
aagggttttg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050  
ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
1 5 10 15  
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn  
20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu  
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn  
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe  
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu  
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser  
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu  
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser  
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu  
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu  
320 325 330

Arg Thr Ser Val

<210> 42  
<211> 1594  
<212> DNA  
<213> Homo sapiens

<400> 42  
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gccttaccgc gcagcccga gattcactat ggtgaaaatc gccttcaata 100  
cccctaccgc cgtgcaaaaag gaggaggcgc ggcaagacgt ggaggccctc 150  
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300  
tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350  
ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400  
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500  
tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600  
aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650  
aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700  
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ttccgccttc gtcgcagaga cctcttgcgt ggtttcaaca aacgtgccat 800  
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
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tcaagatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000  
gaaaaaaaaa aaaactacta accactgcaa gctcttgtca aattttagtt 1050  
taattggcat tgcttggttt ttgaaactga aattacatga gtttcatttt 1100  
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150  
cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200  
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ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400  
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500  
tgtgtaggtg ctgaatgctg taaggagttt aggttgatg aattctacaa 1550  
ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43  
<211> 263  
<212> PRT  
<213> Homo sapiens

<400> 43  
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu  
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg  
20 25 30  
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
35 40 45  
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 44  
 gaaagacacg acacagcagc ttgc 24  
 <210> 45

<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 45  
gggaactgct atotgatgcc 20

<210> 46  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 46  
caggatctcc tcttcagtc tgcagc 26

<210> 47  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 47  
cttctcgaac cacataagtt tgaggcag 28

<210> 48  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 48  
cacgattccc tccacagcaa ctggg 25

<210> 49  
<211> 1969  
<212> DNA  
<213> Homo sapiens

<400> 49  
ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccagggtgcc cccactctcg ctccattcgg 100  
 cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150  
 gtttcggcgg cagccccag cctcctcacc cttctgttgc tgctgctggg 200  
 gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250  
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300  
 ccgagcctcc cgccaccctg gaccccggcc ctccagccca catcgatggg 350  
 gccccagccc acaaccctgg gggggccatc acccccacc aacttcctgg 400  
 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450  
 ggctccctgg cttttctgct gatgttcacg gtctgtgccg cggtcacac 500  
 ccggcagaag cagaaggcct cggcctatta cccatcgctc ttccccaaga 550  
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 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650  
 ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700  
 cccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750  
 ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800  
 agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850  
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900  
 gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950  
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 agtctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050  
 ccccggtat gaaaaggcct tcagccctga ctgcttctg aactccctc 1100  
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 cagaaatgct ggtccccggt gcccggagg aatcttacca agtgccatca 1200  
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 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300  
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350  
 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400  
 aatactgctc ttaattttcc tgaagggtgc cccctgttct tagttggtcc 1450  
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500



caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550  
gatcagggttg aatgaatgga actcttctctg tctggcctcc aaagcagcct 1600  
agaagctgag gggctgtggt tgaggggacc tccaccctgg ggaagtccga 1650  
ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700  
ccacccccctg ttgtcacac attgtctggc agcctgtgtc cacaatattc 1750  
gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800  
ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950  
aaaaaaaaa aaaaaaaga 1969

<210> 50  
<211> 283  
<212> PRT  
<213> Homo sapiens

<400> 50  
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu  
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20 25 30  
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
35 40 45  
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
50 55 60  
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
65 70 75  
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
80 85 90  
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
95 100 105  
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln  
110 115 120  
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
125 130 135  
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
140 145 150  
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr  
 170 175 180  
 Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp  
 185 190 195  
 Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys  
 200 205 210  
 Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro  
 215 220 225  
 Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu  
 230 235 240  
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly  
 245 250 255  
 Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro  
 260 265 270  
 Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val  
 275 280

<210> 51  
 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50  
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100  
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150  
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200  
 cctggcctgc ctctgctgg ccctctgcct gggcagtgagg gaggctggcc 250  
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300  
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350  
 caaagaggcc ggaggggag ctggctctaa agtcagttag gcccttggcc 400  
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450  
 ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500  
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550  
 acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600  
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaagggtg 650  
 ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750  
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800  
 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850  
 gcaaccagaa tgaaggtgc acgaatcccc caccatctgg ctcaggtgga 900  
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950  
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000  
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050  
 agtgggtggca gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100  
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 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250  
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 gaggctcttg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350  
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400  
 tgggatgttt aactttgaca ctttctggaa gaatttttaa tccaagctgg 1450  
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500  
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550  
 cctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600  
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52  
 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys  
 1 5 10 15  
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser  
 20 25 30  
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
 35 40 45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
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<210> 58  
 <211> 1115

<212> PRT  
<213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu	1	5	10	15
Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala	20	25	30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	35	40	45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	50	55	60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	65	70	75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu  
275 280 285

Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met  
290 295 300

Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr  
305 310 315

Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser  
320 325 330

Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu  
335 340 345

Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala  
350 355 360

Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala  
365 370 375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln  
380 385 390

Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln  
395 400 405

Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp  
410 415 420

Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu  
425 430 435

Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg  
440 445 450

Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu  
455 460 465

Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser  
470 475 480

Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro  
485 490 495

Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val  
500 505 510

Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile  
515 520 525

Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu  
530 535 540

Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys  
545 550 555

Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg



					560					565				570
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln
				575					580					585
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp
				590					595					600
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile
				605					610					615
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg
				620					625					630
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys
				635					640					645
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile
				650					655					660
Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly
				665					670					675
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu
				680					685					690
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr
				695					700					705
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr
				710					715					720
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met
				725					730					735
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr
				740					745					750
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys
				755					760					765
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His
				770					775					780'
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn
				785					790					795
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr
				800					805					810
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro
				815					820					825
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg
				830					835					840
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro
				845					850					855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile  
 860 865 870  
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln  
 875 880 885  
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro  
 890 895 900  
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His  
 905 910 915  
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala  
 920 925 930  
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala  
 935 940 945  
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu  
 950 955 960  
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His  
 965 970 975  
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly  
 980 985 990  
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro  
 995 1000 1005  
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys  
 1010 1015 1020  
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg  
 1025 1030 1035  
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro  
 1040 1045 1050  
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu  
 1055 1060 1065  
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp  
 1070 1075 1080  
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly  
 1085 1090 1095  
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr  
 1100 1105 1110  
 Pro Pro Leu Thr Ile  
 1115

<210> 59  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 59  
 gggaaacaca gcagtcattg cctgc 25

<210> 60  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 60  
 gcacacgtag cctgtcgctg gaggc 24

<210> 61  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 61  
 caccaccaag cccagggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
 <211> 1661  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 678  
 <223> unknown base

<400> 62  
 cgggaggctg ggtcgctcatg atccggaccc cattgtcggc ctctgcccatt 50  
 cgccgtgctcc tcccagggtc ccgcggccga cccccgcgca acatgcagcc 100  
 caccggccgc gaggggttccc gcgcgctcag ccggcggtat ctgcggcgtc 150  
 tgctgctcct gctactgctg ctgctgctgc ggcagcccggt aaccgcgcgcg 200  
 gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccccag 250  
 cctcttcacc acgccgggtg tccccagcgc cctcactacc ccaggcctca 300  
 ctacgccagg caccaccaaa accctggacc ttcgggggtcg cgcgcaggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500  
gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
cctactctga actcgagctt gtgacctcag ctgaaggtct gaacagctct 650  
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700  
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750  
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800  
agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850  
agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900  
catcggacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950  
atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000  
tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtga 1050  
cactgtccat gggggtgctg cagtgcaccc tgcttgctaa cgtgtccact 1100  
gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150  
cgggattgggt ggaaattatg acgggactgg ccggttccct caggggctgg 1200  
aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250  
tgagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300  
cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350  
tgagggtga gtttccatat gggcaactga gcacatcctg ccactcccac 1400  
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
gccaaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500  
ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550  
tgctgacaca gtccgtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600  
gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
cacatggaaa a 1661

<210> 63  
<211> 487  
<212> PRT  
<213> Homo sapiens

<220>

<221> unsure

<222> 196, 386

<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg
1				5					10					15
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg
				20					25					30
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
				35					40					45
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
				50					55					60
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro
				65					70					75
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser
				80					85					90
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg
				95					100					105
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe
				110					115					120
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val
				125					130					135
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp
				140					145					150
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His
				155					160					165
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala
				170					175					180
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val
				185					190					195
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser
				200					205					210
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys
				215					220					225
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met
				230					235					240
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
				245					250					255
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu	Glu Val Ser Gln Ala Pro	
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg	Ala Val Cys Asp Asn Leu	
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly	
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu	
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp	His Phe Asp His Ile Arg	
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	
425	430	435
His Leu Val Pro Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro	
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64



ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650  
atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
ctccttctcc ctaacttttag aaatgttgta cttggctatt ttgattaggg 850  
aagaggggatg tgggtctctga tctctgttgt cttcttgggt ctttgggggt 900  
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950  
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
cagctctgag tcttggaat gttgttacct ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gaggaagca tggccagca ttcagcatgt 1100  
gttcctttct gcagtgggtc ttatcaccac ctccctccca gcccggcgc 1150  
ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200  
tgggccccct gagccactg ggtcttcagg gtgcactgga agctggtgtt 1250  
cgctgtcccc tgtgcacttc tcgactggg gcatggagtg cccatgcata 1300  
ctctgtctgcc ggtccctca cctgcacttg aggggtctgg gcagtccctc 1350  
ctctccccag tgtccacagt cactgagcca gacggtcggg tggaacatga 1400  
gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450  
gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550  
ttttatttct ctca 1564

<210> 68  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 68  
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
1 5 10 15  
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
20 25 30  
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
35 40 45  
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60



Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
65 70 75  
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
80 85 90  
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
95 100 105  
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
110 115 120  
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
125 130 135  
Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
140 145 150  
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
155 160 165  
Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
170 175 180  
Met Leu Ser

<210> 69  
<211> 3170  
<212> DNA  
<213> Homo sapiens

<400> 69  
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50  
agttcatagg gtcttgggtc cccgaaccag gaagggttga gggaacacaa 100  
tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150  
tccctttgca ttcccacccc tccgggcttt gcgtcttcct ggggaccccc 200  
tcgccgggag atggccgcgt tgatgcggag caaggattcg tcttgctgcc 250  
tgctcctact ggccgcggtg ctgatgggtg agagctcaca gatcggcagt 300  
tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350  
tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550  
gcatgtgctg cccagtagc cgctgcaata atggcatctg tatcccagtt 600  
actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700  
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800  
tcattttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850  
gtaccaaaca acgcaagaag gggttctcatg ggctggaaat tttccagcgt 900  
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950  
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050  
catggtggaa aataagggtc agatgcagaa gaatggctaa aataagaaac 1100  
gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350  
ttatacaaat aacctacatg ccagatttct attcaacgtt agagttaaac 1400  
aaaatactcc tagaataact tggtatacaa taggttctaa aaataaaatt 1450  
gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550  
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650  
ccacaaatac ttttttttca aaattttagt ttacctgta attaataaga 1700  
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750  
atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800  
aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850  
ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900  
gctaacagag agatcattat ttcttaaaga ttggccataa cctatatattt 1950  
gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000  
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050  
aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150  
tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200  
tcagtgtgag gtctgtgtgc cgtactatcc tcaaattatt tattttatag 2250  
tgctgagatc ctcaaataat ctcaatttca ggagggttca caaaatgtac 2300  
tcttgaagta gacagagtag tgagggttca ttgccctcta taagcttctg 2350  
actagccaat ggcacatcc aattttcttc ccaaacctct gcagcatctg 2400  
ctttattgcc aaagggttag tttcggtttt ctgcagccat tgcggttaaa 2450  
aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500  
accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550  
aactcagttc taaatacttt gtctggagca caaaacaata aaagggttatc 2600  
ttatagtcgt gactttaaac ttttgtagac cacaattcac tttttagttt 2650  
tcttttactt aaatcccac tgcagtctca aatttaagtt ctcccagtag 2700  
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800  
caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850  
tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900  
atataacaat tatttatattt acaatttggg ttctgcaata tttttcttat 2950  
gtccaccctt ttaaaaatta ttatttgaag taatttatat acaggaaatg 3000  
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
taagataaaa tctattaaat ttttctcttc taaaaactga aaaaaaaaaa 3150  
aaaaaaaaa aaaaaaaaaa 3170

<210> 70  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 70  
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu  
1 5 10 15  
Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
20 25 30  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
125 130 135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
140 145 150

Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
155 160 165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
170 175 180

Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
185 190 195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
200 205 210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
215 220 225

Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
230 235 240

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
245 250 255

Cys Gln Lys Ile

<210> 71  
<211> 1809  
<212> DNA  
<213> Homo sapiens

<400> 71  
tctcaatctg ctgacctcgt gatccgcctg accttgtaat ccacctacct 50  
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acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250  
atatttttagt aattcatatg ttttagatta taggttttaa catacttgtg 300  
aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350  
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400  
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550  
ctcaagcccc caacatccca gtccctcagtc ctccagtcac ttgacttcaa 600  
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
agcaccagag ccaggcagtc actgttcctc ctccctggtt ggagtccttt 700  
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800  
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
atacccccag cttctaagat ccagcttct gcagtggaaa tgcctgggtc 900  
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cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000  
aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050  
tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100  
ccgtcattac ctccctgcagt ctgacaagct catcactgaa ttctgctagt 1150  
ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200  
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gatagctcac gtgatgtgga aaacaccagt tggatcaatgg ctcatctgtt 1400  
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tgttattaga aatgtcttaa ccacagcaag aaggagggtg tggctccta 1500  
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ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750  
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
ctgaaaaga 1809

<210> 72  
<211> 363  
<212> PRT  
<213> Homo sapiens

<400> 72  
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile  
1 5 10 15  
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly  
20 25 30  
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys  
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala  
245 250 255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser  
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser  
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln  
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn  
305 310 315

Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr  
320 325 330

Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg  
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp  
350 355 360

Leu Ile Arg

<210> 73  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 73  
aattcatggc aaatatttcc cttccc 26

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 74  
tggtaaactg gcccaaactc gg 22

<210> 75  
<211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
gccgagtggg acaaagcctg gggctgggag ggggccatgg cgctgccatc 50  
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tgactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagggt 200  
caccgacggc ccccgccca ccccgccca ctgggacggc gagaaggagg 250  
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tggaacctta cgcgtcgggc gagcgccgcg cctacggggc ctttttctg 450  
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cagcagctgg gctacgtgct ggccacgctg ctgctcttca tcctgctact 800  
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cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900  
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gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050



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agaggccgcc tccacacccc tccccaggg gcttgggtggc agcatagccc 1250  
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cagccccaaa actgggtgca gcctcagggc aggagtcca ctctccagg 1450  
gctctgctcg tccggggctg ggagatgttc ctggaggagg aactcccat 1500  
cagaacttgg cagccttgaa gttgggtgca gcctcggcag gactccact 1550  
cctcctgggg tgctgcctgc caccaagagc tccccacct gtaccacat 1600  
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tggctgagga caggggaggg agtgaagttg gtttggggtg gcctgtgttg 1900  
ccactctcag cccccacat ttgcatctgc tgggtggacct gccaccatca 1950  
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
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20 25 30  
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His  
80 85 90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His  
95 100 105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg  
110 115 120

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro  
125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu  
140 145 150

Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp  
155 160 165

Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu  
170 175 180

His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala  
185 190 195

Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser  
200 205 210

Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val  
215 220 225

Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln  
230 235 240

Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu  
245 250 255

Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu  
260 265 270

Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn  
275 280 285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg  
290 295 300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu  
305 310 315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp  
320 325 330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys  
335 340

<210> 78  
<211> 2243  
<212> DNA  
<213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150  
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250  
cactgccaag gactactgga tgttcaaact ccgcaactcc tccagcccag 300  
ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350  
taccttgccg ttgcctccac cgtgccctcc atgctgtgcc tggtgggcaa 400  
cttcctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450  
tgacggtcat cctggccatc ttcattggtga taactgcact ggtgaagggtg 500  
gacacttcct cctggaccgg tgggtttttt gcggtcacca ttgtctgcat 550  
ggtgatcctc agcgggtgcct ccactgtctt cagcagcagc atctacggca 600  
tgaccggctc ctttcctatg aggaactccc aagcactgat atcaggagga 650  
gccatgggcg ggacggtcag cgccgtggcc tcattggtgg acttggtgc 700  
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tcttcctcgt gctctgcatg ggactctacc tgctgtgtgc caggctggag 800  
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gattcattga ttccacaca cccctctcc gcccatcct gaagaagacg 950  
gccagcctgg gcttctgtgt cacctacgtc ttcttcatca ccagcctcat 1000  
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cactgtggac caccaagttt ttcattcccc tcaactacct cctcctgtac 1100  
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tcattccccct ctctgtgtgc tgtaactacc agcccccggt ccacctgaag 1250  
actgtggtct tccagtccga tgtgtacccc gcactcctca gctccctgct 1300  
ggggctcagc aacggctacc tcagcaccct ggccctctc tacgggccta 1350  
agattgtgcc caggagctg gctgaggcca cgggagtggg gatgtccttt 1400  
tatgtgtgct tgggcttaac actgggctca gcctgtctta ccctcctggt 1450

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

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Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala
				20					25					30
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
				35					40					45
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
				50					55					60
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
				65					70					75
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
				80					85					90
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
				95					100					105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

[illegible]

				395					400					405
Thr	Val	Val	Phe	Gln 410	Ser	Asp	Val	Tyr	Pro 415	Ala	Leu	Leu	Ser	Ser 420
Leu	Leu	Gly	Leu	Ser 425	Asn	Gly	Tyr	Leu	Ser 430	Thr	Leu	Ala	Leu	Leu 435
Tyr	Gly	Pro	Lys	Ile 440	Val	Pro	Arg	Glu	Leu 445	Ala	Glu	Ala	Thr	Gly 450
Val	Val	Met	Ser	Phe 455	Tyr	Val	Cys	Leu	Gly 460	Leu	Thr	Leu	Gly	Ser 465
Ala	Cys	Ser	Thr	Leu 470	Leu	Val	His	Leu	Ile 475					

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<210> 80
<211> 22
<212> DNA
<213> Artificial
```

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

```
<400> 80
  ttttgcggtc accattgtct gc 22
```

```
<210> 81
<211> 23
<212> DNA
<213> Homo sapiens
```

<220>  
<221> Artificial sequence  
<222> 1-23  
<223> Synthetic construct.

```
<400> 81
cgtaggtgac acagaagccc agg 23
```

```
<210> 82
<211> 49
<212> DNA
<213> Artificial
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<220>  
<221> Artificial sequence  
<222> 1-49  
<223> Synthetic construct.
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<400> 82  
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$$\begin{array}{ll} \langle 210 \rangle & 83 \\ \langle 211 \rangle & 1844 \end{array}$$

<212> DNA  
<213> Homo sapiens

<400> 83  
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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200  
ctatgagcag ctgctcaagg tggcgcctg ggggctcaat cggaccctga 250  
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aaggccact cggccgaaga catctaccag atggctctca accaggccct 650  
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<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165



Leu Gly Tyr Ala	Leu Arg Pro Gln Glu	Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln	Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr Glu			

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala Gly	
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp	Val Glu Thr Ala Val Lys	
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly Pro	
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly	His Ala Ser Asp Met Glu	
515	520	525
Gly Gln Gly His Val His Gly Val Ala	Ser Ser Pro Ser His Asp	
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro	Pro Val Gln Gly Gln Leu	
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg	Thr Ser His	
560	565	

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 tggaggaacc acgagcggg gaagaaggac agggactcgt gtggcaggaa 150  
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
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 cctgacattt ggagctgcca tcttcttgtg gctgatcacc agacctcaac 350  
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 tgtctgacaa tggggccctgc ttgggatata gaaaaccaa ccagccctac 550  
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gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950  
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agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150  
aggtcaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200

ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
				20					25					30

*(Musical notation for Example 6)*

				320					325					330
His	Gln	Asn	Ile	Val 335	Ser	Asn	Ala	Ala	Ala 340	Phe	Leu	Lys	Cys	Val 345
Glu	His	Ala	Tyr	Glu 350	Pro	Thr	Pro	Asp	Asp 355	Val	Ala	Ile	Ser	Tyr 360
Leu	Pro	Leu	Ala	His 365	Met	Phe	Glu	Arg	Ile 370	Val	Gln	Ala	Val	Val 375
Tyr	Ser	Cys	Gly	Ala 380	Arg	Val	Gly	Phe	Phe 385	Gln	Gly	Asp	Ile	Arg 390
Leu	Leu	Ala	Asp	Asp 395	Met	Lys	Thr	Leu	Lys 400	Pro	Thr	Leu	Phe	Pro 405
Ala	Val	Pro	Arg	Leu 410	Leu	Asn	Arg	Ile	Tyr 415	Asp	Lys	Val	Gln	Asn 420
Glu	Ala	Lys	Thr	Pro 425	Leu	Lys	Lys	Phe	Leu 430	Leu	Lys	Leu	Ala	Val 435
Ser	Ser	Lys	Phe	Lys 440	Glu	Leu	Gln	Lys	Gly 445	Ile	Ile	Arg	His	Asp 450
Ser	Phe	Trp	Asp	Lys 455	Leu	Ile	Phe	Ala	Lys 460	Ile	Gln	Asp	Ser	Leu 465
Gly	Gly	Arg	Val	Arg 470	Val	Ile	Val	Thr	Gly 475	Ala	Ala	Pro	Met	Ser 480
Thr	Ser	Val	Met	Thr 485	Phe	Phe	Arg	Ala	Ala 490	Met	Gly	Cys	Gln	Val 495
Tyr	Glu	Ala	Tyr	Gly 500	Gln	Thr	Glu	Cys	Thr 505	Gly	Gly	Cys	Thr	Phe 510
Thr	Leu	Pro	Gly	Asp 515	Trp	Thr	Ser	Gly	His 520	Val	Gly	Val	Pro	Leu 525
Ala	Cys	Asn	Tyr	Val 530	Lys	Leu	Glu	Asp	Val 535	Ala	Asp	Met	Asn	Tyr 540
Phe	Thr	Val	Asn	Asn 545	Glu	Gly	Glu	Val	Cys 550	Ile	Lys	Gly	Thr	Asn 555
Val	Phe	Lys	Gly	Tyr 560	Leu	Lys	Asp	Pro	Glu 565	Lys	Thr	Gln	Glu	Ala 570
Leu	Asp	Ser	Asp	Gly 575	Trp	Leu	His	Thr	Gly 580	Asp	Ile	Gly	Arg	Trp 585
Leu	Pro	Asn	Gly	Thr 590	Leu	Lys	Ile	Ile	Asp 595	Arg	Lys	Lys	Asn	Ile 600
Phe	Lys	Leu	Ala	Gln 605	Gly	Glu	Tyr	Ile	Ala 610	Pro	Glu	Lys	Ile	Glu 615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
				725					730					735

His Ile Gln Asp

<210> 87  
 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
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 caggggccgt gcttttcctg ctggtgactg tcattgtcaa tatcaagttg 300  
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 gaggcagtgg tccccggcgg gtccctggacg tagaggtgta ttcaagtcgc 450  
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500  
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catcggggcc	tgtggagatt	gtttcggaag	aagaaccact	tcctggtggt	2000
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
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 35 40 45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
 50 55 60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
 80 85 90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
 95 100 105  
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
 110 115 120  
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
 125 130 135

Leu	Asn	Gln	Ala	Thr 140	Gly	His	Val	Met	Ala 145	Lys	Arg	Val	Phe	Asp 150
Thr	Tyr	Ser	Pro	His 155	Glu	Asp	Glu	Ala	Met 160	Val	Leu	Phe	Leu	Asn 165
Met	Val	Ala	Pro	Gly 170	Arg	Val	Leu	Ile	Cys 175	Thr	Val	Lys	Asp	Glu 180
Gly	Ser	Phe	His	Leu 185	Lys	Asp	Thr	Ala	Lys 190	Ala	Leu	Leu	Arg	Ser 195
Leu	Gly	Ser	Gln	Ala 200	Gly	Pro	Ala	Leu	Gly 205	Trp	Arg	Asp	Thr	Trp 210
Ala	Phe	Val	Gly	Arg 215	Lys	Gly	Gly	Pro	Val 220	Phe	Gly	Glu	Lys	His 225
Ser	Lys	Ser	Pro	Ala 230	Leu	Ser	Ser	Trp	Gly 235	Asp	Pro	Val	Leu	Leu 240
Lys	Thr	Asp	Val	Pro 245	Leu	Ser	Ser	Ala	Glu 250	Glu	Ala	Glu	Cys	His 255
Trp	Ala	Asp	Thr	Glu 260	Leu	Asn	Arg	Arg	Arg 265	Arg	Arg	Phe	Cys	Ser 270
Lys	Val	Glu	Gly	Tyr 275	Gly	Ser	Val	Cys	Ser 280	Cys	Lys	Asp	Pro	Thr 285
Pro	Ile	Glu	Phe	Ser 290	Pro	Asp	Pro	Leu	Pro 295	Asp	Asn	Lys	Val	Leu 300
Asn	Val	Pro	Val	Ala 305	Val	Ile	Ala	Gly	Asn 310	Arg	Pro	Asn	Tyr	Leu 315
Tyr	Arg	Met	Leu	Arg 320	Ser	Leu	Leu	Ser	Ala 325	Gln	Gly	Val	Ser	Pro 330
Gln	Met	Ile	Thr	Val 335	Phe	Ile	Asp	Gly	Tyr 340	Tyr	Glu	Glu	Pro	Met 345
Asp	Val	Val	Ala	Leu 350	Phe	Gly	Leu	Arg	Gly 355	Ile	Gln	His	Thr	Pro 360
Ile	Ser	Ile	Lys	Asn 365	Ala	Arg	Val	Ser	Gln 370	His	Tyr	Lys	Ala	Ser 375
Leu	Thr	Ala	Thr	Phe 380	Asn	Leu	Phe	Pro	Glu 385	Ala	Lys	Phe	Ala	Val 390
Val	Leu	Glu	Glu	Asp 395	Leu	Asp	Ile	Ala	Val 400	Asp	Phe	Phe	Ser	Phe 405
Leu	Ser	Gln	Ser	Ile 410	His	Leu	Leu	Glu	Glu 415	Asp	Asp	Ser	Leu	Tyr 420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
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Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
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Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu		
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Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr		
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 <212> DNA  
 <213> Artificial  
 <220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.  
 <400> 89



<400> 94

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 ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95  
 <211> 307  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
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 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
 35 40 45  
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
 50 55 60  
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
 65 70 75  
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
 80 85 90  
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
 95 100 105  
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
 110 115 120  
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
 125 130 135  
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
 140 145 150  
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
 155 160 165  
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
 170 175 180  
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
 185 190 195  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
 200 205 210  
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
 215 220 225  
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230		235		240									
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
				245					250					255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
				275					280					285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
				290					295					300

Leu Ser Val Gly His Gln His  
305

<210> 96  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 96  
gttgtgggtg aataaaggag ggcag 25

<210> 97  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 97  
ctgtgctcat gttcatggac aactg 25

<210> 98  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 98  
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99  
<211> 1429



<212> DNA  
<213> Homo sapiens

<400> 99  
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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150  
ccgcccctcg tgctggccgc cctggtggcc tgcattcatcg tcttgggctt 200  
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gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200  
aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250  
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gaaatgtact aaataaaaatg tacatctga 1429

$\langle 210 \rangle$  100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe  
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg  
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg  
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu  
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe  
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val  
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu  
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln  
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg  
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu  
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys  
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp  
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu  
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly  
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser  
230 235 240



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<210> 102  
 <211> 1089  
 <212> PRT  
 <213> Homo sapiens

<400> 102  
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 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu  
 20 25 30  
 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro  
 35 40 45  
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala  
 50 55 60  
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile  
 65 70 75  
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val  
 80 85 90  
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser  
 95 100 105  
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu  
 110 115 120  
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu  
 125 130 135  
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly  
 140 145 150  
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys  
 155 160 165  
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp  
 170 175 180  
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe  
 185 190 195  
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
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Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515		520	525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530		535	540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545		550	555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560		565	570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575		580	585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590		595	600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605		610	615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620		625	630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635		640	645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650		655	660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665		670	675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680		685	690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695		700	705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710		715	720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725		730	735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740		745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755		760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770		775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr



785					790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly
				800					805					810
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala
				815					820					825
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu
				830					835					840
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile
				845					850					855
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu
				860					865					870
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe
				875					880					885
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr
				890					895					900
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile
				905					910					915
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser
				920					925					930
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala
				935					940					945
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp
				950					955					960
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro
				965					970					975
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu
				980					985					990
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe
				995					1000					1005
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu
				1010					1015					1020
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
				1025					1030					1035
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040					1045					1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
				1055					1060					1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
				1070					1075					1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103  
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gcagttccct gtgtctctgg tggtttgccct aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150  
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300  
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350  
taaatcaaac agaacgtggt ccagtggtgt gaccaaccac acgctggtgc 400  
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450  
gtcccagggc ccctcgccg tgetcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550  
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600  
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750  
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800  
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850  
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtccct 950  
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050  
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100  
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200  
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

agccttctga gggggatggg ctcgagagg agggcttct atctagactc 1350  
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400  
 catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450  
 gccaacactt ccttttgct tttgtttcct gtgcaaaca gtgagtcacc 1500  
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550  
 ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600  
 cgtgtgtgat tggttcatgc atgtaggctt cttacaatg atggtgggcc 1650  
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700  
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104  
 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
 Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys  
 1 5 10 15  
 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu  
 20 25 30  
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr  
 35 40 45  
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser  
 50 55 60  
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu  
 65 70 75  
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His  
 80 85 90  
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val  
 95 100 105  
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro  
 110 115 120  
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu  
 125 130 135  
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile  
 140 145 150  
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr  
 155 160 165

118

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct

<400> 105  
cgctgctgct gttgctcctg g 21

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 106  
cagtgtgccca ggactttg 18

<210> 107  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 107  
agtcgcaggc agcgttgg 18

<210> 108  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 108  
ctcctccgag tctgtgtgct cctgc 25

<210> 109  
<211> 51  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

cggacgcgtg ggccggacgcg tgggcccgcg cgtgggtctc tgcggggaga 50  
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100  
tctgctgact gtggccaccg ccctgatgct gcccgtgaag cccccgcag 150  
gctcctgggg ggcccagatc atcgggggccc acgaggtgac cccccactcc 200  
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250  
cttctgctg cgagcccgtt ggggtggtctc ggccgcccac tgcttcagcc 300  
acagagacct ccgactggc ctggtggtgc tgggcgcccac cgtcctgagt 350  
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccatga cccacgcca cgacatctgc ctgctgcggc 450  
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gggagaaggg ccaggcccc caccgcccgg acacggtgcc ggggtggtgg 550  
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gggcttctgc tcggccgact ccggaggggcc cctggtgtgc aggaaccggg 750  
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ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
gccgtccag gcctggaatg ttccgtggct gggcccccac ggaagcctga 1000  
tggtcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
1				5					10					15
Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255





ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250  
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
 tgtcaacgcc cggcacctgg acttggtctt cctcaagtct atccgagagt 400  
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450  
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500  
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 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650  
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 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200  
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250  
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 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450  
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 gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550  
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 ggctgtgccg ggggtgtttg ctgagggtt cctgtgccag agcccagcca 1650

<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
 1 5 10 15  
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
 20 25 30  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
 35 40 45  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
 50 55 60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
 65 70 75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
 80 85 90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
 95 100 105  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
 110 115 120  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
 125 130 135  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
 140 145 150  
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
 155 160 165  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
 170 175 180  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
 185 190 195  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
 200 205 210  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
 215 220 225



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 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
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 cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000  
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050  
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
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 gcaacattta tgatctatct gagctcgggt gaagctggag gagccacagc 1450  
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 acatgagtat ggacaggaat tccgagacc ctgcagctcc agccctgaag 1650  
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700  
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
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 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtggg 1900  
 ggctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950  
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 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
 tagcctgact cccagaactt taagactttc tccccactgc cttctgctgc 2100  
 agccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

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tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	
Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly	185	190	195	
Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu	200	205	210	
Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser	215	220	225	
Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala	230	235	240	

Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser	Val Glu Ala Gly Gly	Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser	Val Pro Val Val Arg	Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His	Arg Ser Gly Glu Gly	Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro	Val Leu Val Gly Asp	Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu	Tyr Gly Gln Glu Phe	Arg Arg Pro Cys Ser Ser			

530

535

540

Ser Pro Glu Asp

<210> 119  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 119  
cgggacagga gacccagaaa ggg 23

<210> 120  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 120  
ggccaagtga tccaaggcat cttc 24

<210> 121  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 121  
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122  
<211> 1778  
<212> DNA  
<213> Homo sapiens

<400> 122  
gagatagggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50  
tccccccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taacccgogc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
gctcaagttt tcaattatca tctattccac cgtgttctgg ctgattgggg 300  
ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400  
ggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550  
gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600  
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
aagtgtctgt gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
cgactgcagt gcccttgac ccctggcctg tggggtgccc tacacctgct 750  
gcatcaggaa cagcagagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
atcgacaagg agcgtttcag tgtgcaggat gtcactctac tgcggggctg 850  
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950  
ctgctgtaca tccccgggt ggaggacatc atcatggagc actctgtcac 1000  
tgatgggctc ctggggcccc gtgccaagcc cagcgtggag gcggcaggca 1050  
cgggatgctg cttgtgctac cccaattagg gccagcctg ccatggcagc 1100  
tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
ggacagggct gcggcccctc tgcccacact cagtactgac caaagccagg 1200  
gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc cccagggagc 1250  
agagcctggg cctcccctaa gaggctttcc ccgaggcagc tctggaatct 1300  
gtgcccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350  
ctacagggga gggagagcct gaggtctgct tcagggccca tttcatctct 1400  
ggcagtgcct tggcggtggt attcaaggca gttttgtagc acctgtaatt 1450  
ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500  
gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccagggttggc 1550  
ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggtgct 1600  
tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650



gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
 gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750  
 catgttttgt tttgttttta aaaaaaaa 1778

<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
 1 5 10 15  
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val  
 20 25 30  
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
 35 40 45  
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60  
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
 65 70 75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
 80 85 90  
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
 95 100 105  
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
 110 115 120  
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
 125 130 135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165  
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
 170 175 180  
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
 185 190 195  
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
 200 205 210  
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
 215 220 225  
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcatctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

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<400> 127
gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgcc tggctcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttctt 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccc tgatcgaggc ttccttcaat 700
ggcatgtatg cagacctcct gcagctggtg aagggtgcca tttccctcag 750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccc ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950
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aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100
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caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggg cccagtgatc ttggtgaagg ccttgggatt cgaggcagct 1450
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<210> 128  
<211> 484  
<212> PRT  
<213> Homo sapiens

<400> 128  
Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala  
1 5 10 15  
Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile  
20 25 30  
Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
35 40 45  
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
50 55 60  
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
65 70 75  
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
80 85 90  
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
95 100 105  
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
110 115 120  
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
125 130 135  
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
140 145 150  
Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
155 160 165  
Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu  
170 175 180  
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
185 190 195  
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
200 205 210  
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
215 220 225

[illegible]

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<210> 129
<211> 2213
<212> DNA
<213> Homo sapiens
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<400> 129  
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gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100  
aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150  
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
agatcctggc aaactcctgg cgataactcca gtgcattcac caacaggata 350  
ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400  
aaacatgaat tcagctccaa ctttcatcaa ctttcttgca aaagggaac 450  
ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500  
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600  
ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650  
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atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800  
tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850  
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900  
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ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050  
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gtatattttg tattacctct ttttttcaag tgatttaa atgttaatcat 1150  
ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200  
ctgaggtatt tgaaaataat tatcctctta accttctctt ccagtggaac 1250  
tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300  
aactactact ttgttttagt tagaacaag ctcaaaacta ctttagtta 1350  
cttggtcatc tgattttata ttgccttacc caaagatggg gaaagtaagt 1400  
cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450

ttcatcttta gcttcttcat ctttgtgtgg atgtgtatac tttacgcac 1500  
 tttccttttg agtagagaaa ttatgtgtgt catgtggtct tctgaaaatg 1550  
 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600  
 ctccctctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650  
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 gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750  
 tccatctcct tagtttttctt ttaaggtgac ccatctgtga taaaaatata 1800  
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 aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900  
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950  
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 tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150  
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200  
 aaaaaaaaaa aaa 2213

<210> 130  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
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 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln  
 20 25 30  
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met  
 35 40 45  
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
 50 55 60  
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile  
 65 70 75  
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys  
 80 85 90  
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg  
 95 100 105





tcagaaccgc taccggcgat gctactgctg tgggtgctcg tggtcgcagc 150  
cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200  
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250  
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300  
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350  
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450  
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aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550  
tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggg 600  
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actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750  
ttcaccatct tctggagaaa attttgatc ttcaacatct cacacatctc 800  
tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850  
tcacctttgt cagaaatgca ccctgtagat tattactctt cttatacaaa 900  
aaactgcact ggaagattta caaaaaaga aattaagaat attagagcat 950  
tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000  
ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050  
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gcatgtacga ggctagtga catgttccgc ttttgatgat gggaccagga 1150  
attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200  
ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250  
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cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450  
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ttctttggat cagaagcttc attcattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600  
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 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
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 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtggctcac 1850  
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 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150  
 tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200  
 aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250  
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300  
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350  
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<210> 132  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
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 1 5 10 15  
 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys  
 20 25 30  
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
 35 40 45  
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
 50 55 60  
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133  
 <211> 1475  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
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 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100  
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200  
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
 catcaccag tgtgacatct atagaccct tctgggctg cccgctgaca 350  
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctccctccctg 400  
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500  
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatac 550  
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650  
 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700  
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750  
 gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
 cagggtatgt gtgaagaacc aggggccaga gctgggggggt ggctgggtct 850  
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900  
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950  
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000  
 attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050  
 gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100  
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150  
 ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200  
 ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250  
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300  
 cctccaaaga aactgattgg ccttgaacc tccatccac tcttgttatg 1350  
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400  
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu  
 1 5 10 15  
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp  
 20 25 30  
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly



atctcccatc tccagtaaact gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggttttt caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
 1 5 10 15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
 65 70 75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
 80 85 90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
 95 100 105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
 110 115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
 ctccactgca accaccaga gccatggctc cccgaggctg catcgtagct 50  
 gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
 agtggcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgtgcc cctggacott catggtgaag ctgataaacc 300  
 agaactgcga ctcagcccg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggccttga gaaagaggct ggtgtttacct gagatctggg atgctgagtg 450  
 gctgttttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
 ggactctgaa cctcctgat gacccttatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
 tatgtacttt ataatgaaa a 771

<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens.

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
 1 5 10 15  
 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met  
 20 25 30  
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp  
 35 40 45  
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val  
 50 55 60  
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg  
 65 70 75  
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu  
 80 85 90  
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu  
 95 100 105  
 Cys Arg Ser Val Ser  
 110

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139



gggggcggggt gcctggagca cggcgctggg gccgcccga gcgctcactc 50  
 gctcgcaactc agtcgcggga ggcttccccg cgcggccgc gtcccgccc 100  
 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
 tctcttccctg gctgcgtccc taggtccggg ggcagccttc aaggctcgca 250  
 cgcgttattc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300  
 tgcaggctct tgggccctgt ggacaaagg cagcatgtga ctttctacaa 350  
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400  
 ggcccatccg caacctcacg ttccaggacc ttacctgca ccatggaggc 450  
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500  
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
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 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650  
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700  
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 ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800  
 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850  
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
 ataccgagg ccaaagtcag gcaccccctg tcctatgtgg cccagcggca 950  
 gccttctgag tctgggcggc atctgcttcc ggagcccagc acccccctgt 1000  
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050  
 gactctccaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150  
 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200  
 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
 atggggatgc tggacggctc agcccctgtt ccaaggattt tggggtgctg 1300  
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500  
 ccccggtggcc gccttggtct ccccggttttg cccgaggctg ctcttctgtc 1550  
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgcctgcca 1600  
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650  
 gatctgtcaa cagggttaagt caatctgggg cttccactgc ctgcattcca 1700  
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750  
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800  
 gttgccccac ccactggaga tgggtgtgag ggaggtgggt ggggccttct 1850  
 gggaaggtga gtggagaggg gcacctgccc cccgccctcc ccattccccta 1900  
 ctccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
 Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly  
 1 5 10 15  
 Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val  
 20 25 30  
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
 35 40 45  
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
 50 55 60  
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
 65 70 75  
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
 80 85 90  
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
 95 100 105  
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
 110 115 120  
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
 125 130 135  
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met Glu
155	160	165
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val Val
170	175	180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala Ala
185	190	195
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro Leu
200	205	210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn Arg
215	220	225
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly Ile
230	235	240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile Pro
245	250	255
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg Gln
260	265	270
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr Pro
275	280	285
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu Asp
290	295	300
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile
305	310	

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 cccacgcgtc cgcgctctc ccttctgctg gaccttcctt cgtctctcca 50  
 tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac 100  
 cttagacctc ccttctgcc ctcttttctt gccacccgtt gcttcttggc 150  
 ccttctccga ccccgctcta gcagcagacc tcctgggggc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250  
 ccgctcccgg accagcggcc tgacctggg gaaaggatgg ttcccgaggt 300  
 gaggtcctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcaccct tacttgagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttggt 500  
 accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
 cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
 ggccccacca aagtccctgcc agcacaacgg gaccatgta' caacacggag 650  
 agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700  
 gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
 ccccgaaacca ggctgcccag caccctccc actgccagac tctgctgcc 800  
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900  
 tgggagaaag agaggcccg gcacccagc cccactggc ctcagcgccc 950  
 ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000  
 actgtcaaga tctcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
 cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100  
 tgggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150  
 tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200  
 agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250  
 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
 ctgctccaca catcgggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
 cctggaacac gaggcctcgg acttggtgga gatctacctc tggaaagtgg 1400  
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
 ccacacagcc agaattctcc acttgactca gatcaagaaa gtcaggaagc 1500  
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggcccccac 1550  
 gaaggctact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
 gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700  
 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
 <211> 451  
 <212> PRT  
 <213> Homo sapiens  
 <400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala  
1 5 10 15  
Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp  
20 25 30  
Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser  
35 40 45  
Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg  
50 55 60  
Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His  
65 70 75  
Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln  
80 85 90  
Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg  
95 100 105  
Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His  
110 115 120  
Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro  
125 130 135  
Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys  
140 145 150  
Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro  
155 160 165  
Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu  
170 175 180  
Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg  
185 190 195  
His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly  
200 205 210  
Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe  
215 220 225  
Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val  
230 235 240  
Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly  
245 250 255  
Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg  
260 265 270  
Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly  
275 280 285  
Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

	290		295		300
Arg His Pro Glu	Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro		
	305		310		315
Glu Asp Lys Ala	Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg		
	320		325		330
Cys Pro Lys Ala	Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser		
	335		340		345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala		
	350		355		360
Ser Asp Leu Val	Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu		
	365		370		375
Glu Thr Glu Ala	Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His		
	380		385		390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala		
	395		400		405
Arg Leu Pro Glu	Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp	Pro		
	410		415		420
Pro Arg Arg Ser	Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly	Ala		
	425		430		435
Glu Gly His Gly	Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr	Lys		
	440		445		450

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
 cttagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50  
 cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100  
 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gtcctcgtt atcgtgaccc cgaggagagcg gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400  
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccgggggtcct 500  
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 ttttaagggtcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
 1 5 10 15  
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
 20 25 30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
 35 40 45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
 50 55 60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
 65 70 75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
 80 85 90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100  
 caggctgcca tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttggtg gagtacatgg 200  
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagaccacaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450  
 tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500  
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600  
 gcaaacagag aagatctacg tgtttagatgg gacacagaat gacacagcct 650  
 ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700  
 gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750  
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
 gagtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
 aaccgaacag tgggtggacag ctcaagtatt ccagcagagg ggctgatccc 900  
 cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
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 tcctttgatg ccagcggcac cctgaccct gaacgggcag cactccctta 1200  
 ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
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 ttcctcattc ttcaaagtgt ggccagttgt ggctcaaac ctctatatatt 1450  
 ttagccaatg gcaatcaaat tctttcagct cttttgtttc atacggaaact 1500  
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
 ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600  
 cccagacca gggctctaac cttgtatgcg ggcaggcca gggagcaggc 1650  
 agcagtgttc ttcccctcag agtgacttgg ggaggagagaa ataggaggag 1700  
 acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750  
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850





Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala  
260 265 270  
Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala  
275 280 285  
Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys  
290 295 300  
Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro  
305 310 315  
Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr  
320 325 330  
Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile  
335 340 345  
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala  
350 355 360  
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu  
365 370 375  
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly  
380 385 390  
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu  
395 400 405

Val

<210> 147  
<211> 2052  
<212> DNA  
<213> Homo sapiens

<400> 147  
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gttctcctct tctctcta atccatccgtca cctctcctgt catccgtttc 150  
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
ttgggttctga gtctcctcaa gctgggatca gggcagtggc aggtgttttg 250  
gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
attctattgc ggaggggacg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550  
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tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650  
tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700  
ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750  
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tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagat 850  
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aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050  
tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg 1100  
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
aacattactg ggaggtggac ggaggacaca ataaaaggtg gcgcgtggga 1250  
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cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
cattaaatcc ccgttttata agcgtcttcc ccaggacccc acctacaaaa 1400  
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tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaaactccc 1550  
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aagggcctct gcaatcccag agacaagcaa cagtgagtcc tctcacagg 1650  
caaccacgcc ctctctccc aggggtgaaa tgtaggatga atcacatccc 1700  
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cattacattt agtttctct cactccatct ggctaagtga tcttgaaata 1900  
ccacctctca ggtgaagaac cgtcaggaat tccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000

acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050

aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly
1				5					10					15

Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala
				20					25					30

Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
				35					40					45

Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
				50					55					60

Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
				65					70					75

Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
				80					85					90

Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
				95					100					105

Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
				110					115					120

Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
				125					130					135

Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
				140					145					150

Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
				155					160					165

Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
				170					175					180

Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
				185					190					195

Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
				200					205					210

Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
				215					220					225

Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149  
<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggettcctt 50  
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250  
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
gggcgacggc tcccacggcc caggccccga ggaccgggccc ccgcgcgcc 350  
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
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acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550  
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600  
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gccatgtgac tgtagtcac atggagctct cagcataccg tgcaacaggt 900  
aagcaacaga gggtggaact gaagtttatt ttattttagc aagggaaaaa 950  
aaaaggctgc tactctcaag gaccatactg gtttaaacia aggaggatga 1000  
gggtcataga ttacaaaat attttatata cttttattct cttactttat 1050  
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100  
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150  
atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggct 1200  
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atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300  
taatcaaat tctacatttg tttcttgga catctaaagc ttaacctggg 1350  
ggtaccctaa tttatttaac tagtggaag tagactggtt ttactctatt 1400  
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500  
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ctgggttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

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actaaatatt	ttaaagtgctt	tataaatgat	attatactgt	tatggaatat	1950
tgtatcatat	tgtagtttat	taaaaatgta	gaagaggctg	ggcgcggtgg	2000
ctcacgcctg	taatcctagc	actttgggag	gccaaggcgg	gtggatcact	2050
tgaggccagg	agttctagat	gagcctggcc	agcacagtga	aaccccgctct	2100
ctactaaaaa	tacaaacaaa	ttagctgggc	gtggtggcac	acacctgtag	2150
tcccagctac	tcgggaggct	gaggcaggag	aatcggttga	acccgggagg	2200
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<210> 153
<211> 258
<212> PRT
<213> Homo sapiens
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<400>	153													
Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro





<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtaggcctc 150  
 ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200  
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgccca tcattctcac tcagctggag 400  
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttctctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600  
 gggctcctgtg acctcggcca gtgtccaccc acctcgctca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
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 gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa 100  
 gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150  
 gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttaccc 200  
 tggcccagta gttcatggct actgggttcg ggaaggggcc aatacagacc 250  
 aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300  
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
 gtatggagaa aggaagtata aatggaatt ataaacatca ccggctctct 450  
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
 gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600  
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcaccccaca 650  
 gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
 tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900  
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

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<210> 160
<211> 463
<212> PRT
<213> Homo sapiens
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<400>	160													
Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	110	115	120
125 130 135			
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala  
 410 415 420  
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser  
 425 430 435  
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu  
 440 445 450  
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg  
 455 460

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100  
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttcggag gacaggaggc ccaggaaggt gtccccagtg 200  
 aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250  
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400  
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550  
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650  
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
 1 5 10 15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg	20	25	30
				35					40					45			
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly			
				50					55					60			
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile			
				65					70					75			
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr			
				80					85					90			
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro			
				95					100					105			
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly			
				110					115					120			
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr			
				125					130					135			
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys			
				140					145					150			
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser			
				155					160					165			
Cys	Val	Pro	Glu	His													
				170													

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.

<400> 165  
gtcctccgga aagtccttat c 21

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 166  
gcctagtgtt cggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 167  
caggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 168  
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169



gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150  
gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200  
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250  
cgacgtcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300  
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350  
ctgtgagcag acccggacag ccactgagtc cttccccac ccgggttca 400  
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500  
ctcacgtgtg gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600  
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650  
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800  
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850  
acaattagac tggaccacc caccacagcc catcaccctc catttccact 900  
tgggtgtttg ttctgttca ctctgttaat aagaaaccct aagccaagac 950  
cctctacgaa cattctttg gccctctgga ctacaggaga tgctgtcact 1000  
taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050  
ccttgaaata ttgtgactct gggaatgaca acacctggtt tggttctctgt 1100  
tgtatcccca gcccacaaaga cagctcctgg ccatatatca aggtttcaat 1150  
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
aaaa 1204

<210> 170  
<211> 250  
<212> PRT  
<213> Homo sapiens

<400> 170  
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	
				20					25					30	
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	
				35					40					45	
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	
				50					55					60	
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	
				65					70					75	
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	
				80					85					90	
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	
				95					100					105	
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.



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<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 176
cccttgatga tcctgggc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150
agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaaatgaag gccaccccaa atgggttggt cttgggtgtg ggcaagtc 300
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

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ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
 tgtgaccaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
 ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750  
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850  
 ttgcaaacctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
 aaaaaaa 907

<210> 180  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe  
 1 5 10 15  
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu  
 20 25 30  
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn  
 35 40 45  
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr  
 50 55 60  
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg  
 65 70 75  
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly  
 80 85 90  
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro  
 95 100 105  
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly  
 110 115 120  
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu  
 125 130 135  
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser  
 140 145 150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu  
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys  
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu  
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser  
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu  
215 220

<210> 181  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 181  
gtgttctgct ggagccgatg cc 22

<210> 182  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 182  
gacatggaca atgacagg 18

<210> 183  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 183  
cctttcagga tgtaggag 18

<210> 184  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 184  
 gatgtctgcc accccaag 18

<210> 185  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 185  
 gcatcctgat atgacttgct acgtggc 27

<210> 186  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 186  
 tacaagaggg aagaggagtt gcac 24

<210> 187  
 <211> 52  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-52  
 <223> Synthetic construct.

<400> 187  
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
 cc 52

<210> 188  
 <211> 573  
 <212> DNA  
 <213> Homo sapiens

<400> 188  
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50  
 ctctttggag ctgtgactca gaaaacaaa acttcctgtg ctaagtgcc 100

atactttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200  
aagccaggc atgggtggctc ggcctgttaa tcccagttct ttgggaagcc 250  
aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350  
ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
ttcttgtttc atttcgcgac tgccctctca gtgtttcttg ggatcccctc 550  
ccaaataaag tacttatatt ctc 573

<210> 189  
<211> 74  
<212> PRT  
<213> Homo sapiens

<400> 189  
Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser  
1 5 10 15  
Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
20 25 30  
Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
35 40 45  
Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
50 55 60  
Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
65 70

<210> 190  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 190  
agggaccatt gcttcttcca ggcc 24

<210> 191  
<211> 24  
<212> DNA  
<213> Artificial



<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 191  
 cgttacatgt ctccaagggg aatg 24

<210> 192  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 192  
 cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193  
 <211> 1091  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
 caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
 ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
 gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150  
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
 gtgtgggctg aactcacagc cgtggcaggc ggggctgttt gagggcacca 250  
 gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
 gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350  
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
 cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450  
 ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500  
 gccctgccc aatgactgtg caaccgctgg caccgagtgc caggtctcag 550  
 gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
 tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
 cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700  
 atgcctgcca gggtgattct gggggcccc tggtgtgtgg gggagtcctt 750  
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000  
 gccagccctt ctaagaccca cgagcggggg gagagaagtg tgcaatagtc 1050  
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194  
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser  
     1                    5                    10                    15  
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg  
                     20                    25                    30  
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu  
                     35                    40                    45  
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala  
                     50                    55                    60  
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His  
                     65                    70                    75  
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly  
                     80                    85                    90  
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His  
                     95                    100                    105  
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val  
                     110                    115                    120  
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr  
                     125                    130                    135  
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His  
                     140                    145                    150  
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser  
                     155                    160                    165  
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile  
                     170                    175                    180  
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala  
                     185                    190                    195  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val	Gly Pro Cys Gly Gln Asp	
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile	Cys Lys Tyr Val Asp Trp	
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
 gcggccacac gcagctagcc ggagcccga ccaggcgcct gtgcctcctc 50  
 ctgcctcctc gccgcgtccg cgaagcctgg agccggcgagg agccccgcgc 100  
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150  
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350  
 caagaccac ctggagatga agaagatgat ctgagagggt acaggagggg 400  
 tcagtgcacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450  
 cggtcggtg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500  
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550  
 tgccctgagg acccgcctg gactccccag ccttcccacc ccatacctcc 600  
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650  
 tttgtttggt cattgagggt ttgtttgtgt tttcatcaat gtctttgtaa 700  
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 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
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Ile Leu Val Thr	Ser Phe Asn His Met	Pro Lys Ile Arg Thr	Leu
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215		220	225
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Leu Cys Met Ala	Pro Val His Leu Arg	Gly Phe Asn Val Ala	Asp
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260		265	270
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Ile Pro Ala Asn	Leu Pro Glu Gly Ile	Val Glu Ile Arg Leu	Glu
305		310	315
Gln Asn Ser Ile	Lys Ala Ile Pro Ala	Gly Ala Phe Thr Gln	Tyr
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Lys Lys Leu Lys	Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser	Asp
335		340	345
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Val Leu Tyr Gly	Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu	Phe
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Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
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Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
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Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
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Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
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Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
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Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
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Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
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Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
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Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
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Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr  
755 760 765

Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile  
770 775 780

Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe  
785 790 795

Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg  
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Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu  
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Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu  
830 835 840

Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly  
845 850 855

Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu  
860 865 870

Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser  
875 880 885

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His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala  
905 910 915

Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr  
920 925 930

Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr  
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Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile  
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Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser  
965 970 975

His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly  
980 985 990

Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys  
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Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys  
1010 1015 1020

Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile  
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Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

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1310					1315					1320				
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1325					1330					1335				

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1370 1375 1380

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1385 1390 1395

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Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
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Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
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Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
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Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys	Lys	His	Cys	Glu	Gly
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Arg	Asp	Leu	Ser	Glu	Trp	Lys	Lys	Gly	Cys	Glu	Val	Ser		
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<400> 204
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<210> 206
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<212> DNA
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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
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<210> 207
<211> 24
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<220>
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<222> 1-24
<223> Synthetic construct.

<400> 207
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<210> 208
<211> 47
<212> DNA
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<220>
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<223> Synthetic construct.

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gcggaagaag atcctattht actgtcactt cccagatctg cttctcacca 250

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tactgtcat ctgttaggga atttttgttt gtccctgtct tgccctggatc 1550  
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<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg  
 275 280 285  
 Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg  
 290 295 300  
 Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr  
 305 310 315  
 Arg Tyr Val Thr Lys Leu Leu Val  
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<210> 211  
 <211> 1554  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
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 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgggaa 200  
 tttgcatgag ttctctggtta atttgcata gagatatggg cctgtggtct 250  
 ccttctggtt tggcaggcgc ctctggttga gtttgggcac tgttgatgta 300  
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400  
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg ctccagaag aatcatggca cagtttggtc 650  
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 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
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 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
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gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250  
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cagtacttct tagtgatttg gtgaagagac tgcacctact ttctgtggag 1350  
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agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
ttaa 1554

<210> 212  
<211> 462  
<212> PRT  
<213> Homo sapiens

<400> 212  
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Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala  
20 25 30  
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu  
35 40 45  
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn  
50 55 60  
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg  
65 70 75  
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His  
80 85 90  
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys  
95 100 105  
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn  
110 115 120  
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu  
125 130 135  
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser
155	160 165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val
170	175 180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln
185	190 195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu
200	205 210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu
215	220 225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys
230	235 240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser
245	250 255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser
260	265 270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys
275	280 285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys
290	295 300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val
305	310 315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu
320	325 330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln
335	340 345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg
350	355 360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro
365	370 375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp
380	385 390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly
395	400 405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr
410	415 420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val
425	430 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
455 460

<210> 213  
<211> 759  
<212> DNA  
<213> Homo sapiens

<400> 213  
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tcagggtctg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150  
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
ctctcacgtt caccctcgag gagtatgaca agcaggacat tcagctggtg 250  
gccgcgtct ctgtcacctt gggcctcttt gcagtggagc tggccggttt 300  
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
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tgaggagtgc ctacgtattg gtacattttt gtctcttgca gtgcccttcc 450  
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
aaccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
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ttccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaaa 750  
aaaaaaaaa 759

<210> 214  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 214  
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
1 5 10 15  
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
20 25 30  
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
50 55 60  
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
65 70 75  
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
80 85 90  
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
95 100 105  
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
110 115 120  
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
125 130 135  
Lys Lys Lys Pro Phe  
140

<210> 215  
<211> 697  
<212> DNA  
<213> Homo sapiens

<400> 215  
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gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150  
ggcatcagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200  
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caggcccgga atgtgcagca ctaccacatg aagacactgg gctgggtgca 300  
cgtgggctac aacttctga ttggagaaga cgggctcgta tacgagggcc 350  
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
tccattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450  
ccaggccatc cgggcagccc agggcttact ggctgcgggt gtggctcagg 500  
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
ctaccgctcc cctgaggcc ctgctgatcc gcacccatt cctccctcc 650  
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216  
<211> 196  
<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	1	5	10	15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	20	25	30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	35	40	45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	50	55	60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	65	70	75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	80	85	90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	95	100	105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	110	115	120	
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	125	130	135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	140	145	150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	155	160	165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	170	175	180	
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser	185	190	195	

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150

cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcgaa 200



gcggggccac atctcaccta agtccccccc catggccaat tccactctcc 250  
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300  
cccaaccgcc cgaaccacag cccccacccc tcagccaagg tgaagaaaat 350  
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400  
tgctcgtcac aggggaagatt gtggaccatg gcaatgggac cttcagcgtc 450  
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gaacggggcc gccggacctc gctttgcacc cagacccag ccaagatctg 650  
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cccatctggg tgaccggggg caggccacag agggcaggcc agggctggaa 850  
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aataaagctt gccccggggc a 1871

<210> 218  
<211> 252  
<212> PRT  
<213> Homo sapiens

<400> 218  
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Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser  
20 25 30  
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg  
35 40 45  
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met  
50 55 60  
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala  
65 70 75  
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro  
80 85 90  
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe  
95 100 105  
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly  
110 115 120  
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln  
125 130 135  
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro  
140 145 150  
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile  
155 160 165  
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu  
170 175 180  
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro  
185 190 195  
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp  
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
245 250

<210> 219  
<211> 2065  
<212> DNA  
<213> Homo sapiens

<400> 219  
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ccggggcgctg tccgcgggtgc cggccgtgct gctggtcctc acgctgccgg 400  
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tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750  
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ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000  
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
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tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
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<212> PRT  
<213> Homo sapiens

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35 40 45  
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
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Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
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Phe	Leu	Val	Phe	Pro	Leu										
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<210> 221  
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 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-20  
 <223> Synthetic construct.

<400> 221  
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 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
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 <223> Synthetic construct,

<400> 222  
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<210> 223  
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<212> DNA  
 <213> Artificial

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 <223> Synthetic construct.

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<210> 224  
 <211> 902  
 <212> DNA  
 <213> Homo sapiens

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 tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150  
 tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200  
 ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
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 tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850  
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 ta 902

<210> 225  
 <211> 257  
 <212> PRT

<213> Homo sapiens

<400> 225

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				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
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Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
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Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
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Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
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<210> 226

<211> 3939  
 <212> DNA  
 <213> Homo sapiens

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 <211> 832  
 <212> PRT  
 <213> Homo sapiens

<400> 227  
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Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser
				35					40					45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn
				50					55					60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln
				65					70					75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val
				80					85					90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg
				95					100					105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro
				110					115					120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser
				125					130					135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg
				140					145					150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn
				155					160					165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu
				170					175					180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe
				185					190					195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr
				200					205					210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met
				215					220					225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser
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Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala
				245					250					255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro
				260					265					270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser
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Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys
				290					295					300
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				335					340					345					
Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly					
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Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser					
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Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala					
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Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe					
				440					445					450					
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val					
				455					460					465					
Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn					
				470					475					480					
Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly					
				485					490					495					
Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile					
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Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile					
				515					520					525					
Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu					
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Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr					
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Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys					
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Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met					
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Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro					
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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				20						25					30
Glu	Asn	Tyr	Gly	Gly 35	Asn	Phe	Pro	Leu	Tyr 40	Leu	Thr	Lys	Leu	Pro 45	
Leu	Pro	Arg	Glu	Gly 50	Ala	Glu	Gly	Gln	Ile 55	Val	Leu	Ser	Gly	Asp 60	
Ser	Gly	Lys	Ala	Thr 65	Glu	Gly	Pro	Phe	Ala 70	Met	Asp	Pro	Asp	Ser 75	
Gly	Phe	Leu	Leu	Val 80	Thr	Arg	Ala	Leu	Asp 85	Arg	Glu	Glu	Gln	Ala 90	
Glu	Tyr	Gln	Leu	Gln 95	Val	Thr	Leu	Glu	Met 100	Gln	Asp	Gly	His	Val 105	
Leu	Trp	Gly	Pro	Gln 110	Pro	Val	Leu	Val	His 115	Val	Lys	Asp	Glu	Asn 120	
Asp	Gln	Val	Pro	His 125	Phe	Ser	Gln	Ala	Ile 130	Tyr	Arg	Ala	Arg	Leu 135	
Ser	Arg	Gly	Thr	Arg 140	Pro	Gly	Ile	Pro	Phe 145	Leu	Phe	Leu	Glu	Ala 150	
Ser	Asp	Arg	Asp	Glu 155	Pro	Gly	Thr	Ala	Asn 160	Ser	Asp	Leu	Arg	Phe 165	
His	Ile	Leu	Ser	Gln 170	Ala	Pro	Ala	Gln	Pro 175	Ser	Pro	Asp	Met	Phe 180	
Gln	Leu	Glu	Pro	Arg 185	Leu	Gly	Ala	Leu	Ala 190	Leu	Ser	Pro	Lys	Gly 195	
Ser	Thr	Ser	Leu	Asp 200	His	Ala	Leu	Glu	Arg 205	Thr	Tyr	Gln	Leu	Leu 210	
Val	Gln	Val	Lys	Asp 215	Met	Gly	Asp	Gln	Ala 220	Ser	Gly	His	Gln	Ala 225	
Thr	Ala	Thr	Val	Glu 230	Val	Ser	Ile	Ile	Glu 235	Ser	Thr	Trp	Val	Ser 240	
Leu	Glu	Pro	Ile	His 245	Leu	Ala	Glu	Asn	Leu 250	Lys	Val	Leu	Tyr	Pro 255	
His	His	Met	Ala	Gln 260	Val	His	Trp	Ser	Gly 265	Gly	Asp	Val	His	Tyr 270	
His	Leu	Glu	Ser	His 275	Pro	Pro	Gly	Pro	Phe 280	Glu	Val	Asn	Ala	Glu 285	
Gly	Asn	Leu	Tyr	Val 290	Thr	Arg	Glu	Leu	Asp 295	Arg	Glu	Ala	Gln	Ala 300	
Glu	Tyr	Leu	Leu	Gln 305	Val	Arg	Ala	Gln	Asn 310	Ser	His	Gly	Glu	Asp 315	



Tyr	Ala	Ala	Pro	Leu 320	Glu	Leu	His	Val	Leu 325	Val	Met	Asp	Glu	Asn 330
Asp	Asn	Val	Pro	Ile 335	Cys	Pro	Pro	Arg	Asp 340	Pro	Thr	Val	Ser	Ile 345
Pro	Glu	Leu	Ser	Pro 350	Pro	Gly	Thr	Glu	Val 355	Thr	Arg	Leu	Ser	Ala 360
Glu	Asp	Ala	Asp	Ala 365	Pro	Gly	Ser	Pro	Asn 370	Ser	His	Val	Val	Tyr 375
Gln	Leu	Leu	Ser	Pro 380	Glu	Pro	Glu	Asp	Gly 385	Val	Glu	Gly	Arg	Ala 390
Phe	Gln	Val	Asp	Pro 395	Thr	Ser	Gly	Ser	Val 400	Thr	Leu	Gly	Val	Leu 405
Pro	Leu	Arg	Ala	Gly 410	Gln	Asn	Ile	Leu	Leu 415	Leu	Val	Leu	Ala	Met 420
Asp	Leu	Ala	Gly	Ala 425	Glu	Gly	Gly	Phe	Ser 430	Ser	Thr	Cys	Glu	Val 435
Glu	Val	Ala	Val	Thr 440	Asp	Ile	Asn	Asp	His 445	Ala	Pro	Glu	Phe	Ile 450
Thr	Ser	Gln	Ile	Gly 455	Pro	Ile	Ser	Leu	Pro 460	Glu	Asp	Val	Glu	Pro 465
Gly	Thr	Leu	Val	Ala 470	Met	Leu	Thr	Ala	Ile 475	Asp	Ala	Asp	Leu	Glu 480
Pro	Ala	Phe	Arg	Leu 485	Met	Asp	Phe	Ala	Ile 490	Glu	Arg	Gly	Asp	Thr 495
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His	Glu	Val	Val	Val 530	Val	Val	Gln	Ser	Val 535	Ala	Lys	Leu	Val	Gly 540
Pro	Gly	Pro	Gly	Pro 545	Gly	Ala	Thr	Ala	Thr 550	Val	Thr	Val	Leu	Val 555
Glu	Arg	Val	Met	Pro 560	Pro	Pro	Lys	Leu	Asp 565	Gln	Glu	Ser	Tyr	Glu 570
Ala	Ser	Val	Pro	Ile 575	Ser	Ala	Pro	Ala	Gly 580	Ser	Phe	Leu	Leu	Thr 585
Ile	Gln	Pro	Ser	Asp 590	Pro	Ile	Ser	Arg	Thr 595	Leu	Arg	Phe	Ser	Leu 600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val	
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile	
770	775	780
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Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr Val	
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 <212> DNA  
 <213> Artificial Sequence

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<400> 231  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 233  
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 <212> DNA  
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 acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
 gatgtcctgg tcccatctgt cagtctgcag gcatttaaact ccttcctgag 250  
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<210> 234  
 <211> 421  
 <212> PRT  
 <213> Homo sapiens

<400> 234  
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 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn  
 35 40 45  
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe  
 50 55 60  
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala  
 65 70 75  
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr  
 80 85 90  
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met  
 95 100 105  
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr  
 110 115 120  
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn  
 125 130 135  
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly  
 140 145 150  
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr  
 155 160 165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	
				170					175					180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	
				185					190					195	
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	
				200					205					210	
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	
				215					220					225	
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	
				230					235					240	
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	
				245					250					255	
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	
				260					265					270	
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	
				275					280					285	
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	
				290					295					300	
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	
				305					310					315	
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	
				320					325					330	
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	
				335					340					345	
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	
				350					355					360	
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	
				365					370					375	
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
				380					385					390	
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	
				395					400					405	
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	
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Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
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 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr  
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 35 40 45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
 50 55 60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
 65 70 75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
 80 85 90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
 95 100 105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
 110 115 120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
 125 130 135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
 140 145 150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
 155 160 165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
 170 175 180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
 185 190 195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala



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Lys Trp Glu Lys Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe	
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Pro Phe Leu Val Gly Glu Gln Val Thr	Val Gln Val Pro Met Met	
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn	
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe	
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala	
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys	
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser	
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala	
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser	
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser	
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile	
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn	
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile	
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro	Thr Lys Ser	
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.  
  
 <400> 238  
 ctttgctggtt ggccctctgtg ctcccaacca tgcaaggaca gggcagg 47  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 239  
 tgactcgggg tctccaaaac cagc 24  
  
 <210> 240  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 240  
 ggtataggcg gaaggcaaag tcgg 24  
  
 <210> 241  
 <211> 48  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.  
  
 <400> 241  
 ggcattctac ctttatggag tactctttgc tgttggcctc tgtgctcc 48  
  
 <210> 242  
 <211> 2436  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 242  
 ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

229

caactctgac tccagcacia cctccagtga ggccagcaca gccaccaact 1550  
ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag 1600  
tccagcacia cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650  
tgtgacctct gcaggctctg gaacagcagc tctgactgga atgcacacia 1700  
cttcccatag tgcattctact gcagtgagtg aggcaaagcc tgggtgggtcc 1750  
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cgtggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850  
tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaaccat 1900  
ggccttggtc caggccctgg agggaatcat ggagcccccc acaggcccag 1950  
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agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050  
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cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150  
tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200  
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250  
acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300  
gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350  
tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243  
<211> 596  
<212> PRT  
<213> Homo sapiens

<400> 243  
Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu  
1 5 10 15  
Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser  
20 25 30  
Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala  
35 40 45  
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala  
50 55 60  
Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val  
65 70 75

Thr	Asn	Ser	Glu	Phe 80	His	Thr	Thr	Ser	Ser 85	Gly	Ile	Ser	Thr	Ala 90
Thr	Asn	Ser	Glu	Phe 95	Ser	Thr	Ala	Ser	Ser 100	Gly	Ile	Ser	Ile	Ala 105
Thr	Asn	Ser	Glu	Ser 110	Ser	Thr	Thr	Ser	Ser 115	Gly	Ala	Ser	Thr	Ala 120
Thr	Asn	Ser	Glu	Ser 125	Ser	Thr	Pro	Ser	Ser 130	Gly	Ala	Ser	Thr	Val 135
Thr	Asn	Ser	Gly	Ser 140	Ser	Val	Thr	Ser	Ser 145	Gly	Ala	Ser	Thr	Ala 150
Thr	Asn	Ser	Glu	Ser 155	Ser	Thr	Val	Ser	Ser 160	Arg	Ala	Ser	Thr	Ala 165
Thr	Asn	Ser	Glu	Ser 170	Ser	Thr	Leu	Ser	Ser 175	Gly	Ala	Ser	Thr	Ala 180
Thr	Asn	Ser	Asp	Ser 185	Ser	Thr	Thr	Ser	Ser 190	Gly	Ala	Ser	Thr	Ala 195
Thr	Asn	Ser	Glu	Ser 200	Ser	Thr	Thr	Ser	Ser 205	Gly	Ala	Ser	Thr	Ala 210
Thr	Asn	Ser	Glu	Ser 215	Ser	Thr	Val	Ser	Ser 220	Arg	Ala	Ser	Thr	Ala 225
Thr	Asn	Ser	Glu	Ser 230	Ser	Thr	Thr	Ser	Ser 235	Gly	Ala	Ser	Thr	Ala 240
Thr	Asn	Ser	Glu	Ser 245	Arg	Thr	Thr	Ser	Asn 250	Gly	Ala	Gly	Thr	Ala 255
Thr	Asn	Ser	Glu	Ser 260	Ser	Thr	Thr	Ser	Ser 265	Gly	Ala	Ser	Thr	Ala 270
Thr	Asn	Ser	Asp	Ser 275	Ser	Thr	Val	Ser	Ser 280	Gly	Ala	Ser	Thr	Ala 285
Thr	Asn	Ser	Glu	Ser 290	Ser	Thr	Thr	Ser	Ser 295	Gly	Ala	Ser	Thr	Ala 300
Thr	Asn	Ser	Glu	Ser 305	Ser	Thr	Thr	Ser	Ser 310	Gly	Ala	Ser	Thr	Ala 315
Thr	Asn	Ser	Asp	Ser 320	Ser	Thr	Thr	Ser	Ser 325	Gly	Ala	Gly	Thr	Ala 330
Thr	Asn	Ser	Glu	Ser 335	Ser	Thr	Val	Ser	Ser 340	Gly	Ile	Ser	Thr	Val 345
Thr	Asn	Ser	Glu	Ser 350	Ser	Thr	Pro	Ser	Ser 355	Gly	Ala	Asn	Thr	Ala 360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

				365					370					375
Thr	Asn	Ser	Glu	Ser 380	Ser	Thr	Val	Ser	Ser 385	Gly	Ala	Ser	Thr	Ala 390
Thr	Asn	Ser	Glu	Ser 395	Ser	Thr	Thr	Ser	Ser 400	Gly	Val	Ser	Thr	Ala 405
Thr	Asn	Ser	Glu	Ser 410	Ser	Thr	Thr	Ser	Ser 415	Gly	Ala	Ser	Thr	Ala 420
Thr	Asn	Ser	Asp	Ser 425	Ser	Thr	Thr	Ser	Ser 430	Glu	Ala	Ser	Thr	Ala 435
Thr	Asn	Ser	Glu	Ser 440	Ser	Thr	Val	Ser	Ser 445	Gly	Ile	Ser	Thr	Val 450
Thr	Asn	Ser	Glu	Ser 455	Ser	Thr	Thr	Ser	Ser 460	Gly	Ala	Asn	Thr	Ala 465
Thr	Asn	Ser	Gly	Ser 470	Ser	Val	Thr	Ser	Ala 475	Gly	Ser	Gly	Thr	Ala 480
Ala	Leu	Thr	Gly	Met 485	His	Thr	Thr	Ser	His 490	Ser	Ala	Ser	Thr	Ala 495
Val	Ser	Glu	Ala	Lys 500	Pro	Gly	Gly	Ser	Leu 505	Val	Pro	Trp	Glu	Ile 510
Phe	Leu	Ile	Thr	Leu 515	Val	Ser	Val	Val	Ala 520	Ala	Val	Gly	Leu	Phe 525
Ala	Gly	Leu	Phe	Phe 530	Cys	Val	Arg	Asn	Ser 535	Leu	Ser	Leu	Arg	Asn 540
Thr	Phe	Asn	Thr	Ala 545	Val	Tyr	His	Pro	His 550	Gly	Leu	Asn	His	Gly 555
Leu	Gly	Pro	Gly	Pro 560	Gly	Gly	Asn	His	Gly 565	Ala	Pro	His	Arg	Pro 570
Arg	Trp	Ser	Pro	Asn 575	Trp	Phe	Trp	Arg	Arg 580	Pro	Val	Ser	Ser	Ile 585
Ala	Met	Glu	Met	Ser 590	Gly	Arg	Asn	Ser	Gly 595	Pro				

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<210> 244
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 244
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gaagcaccag cctttatctc ttcacc 26

<210> 245  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic sequence.

<400> 245  
 gtcagagttg gtggctgtgc tagc 24

<210> 246  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 246  
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247  
 <211> 957  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
 gggagagagg ataaatagca gcggtggcttc cctggctcct ctctgcatcc 50  
 ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100  
 tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150  
 cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200  
 agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
 ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
 tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaaag 400  
 gaagcagaga agcttggcca tggggtcaac aacgctgctg gacaggcccg 450  
 gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500  
 ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550  
 caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800  
acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900  
tttttgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950  
tacacca 957

<210> 248  
<211> 247  
<212> PRT  
<213> Homo sapiens

<400> 248  
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu  
1 5 10 15  
Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu  
20 25 30  
Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg  
35 40 45  
Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His  
50 55 60  
Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met  
65 70 75  
Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu  
80 85 90  
Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile  
95 100 105  
Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn  
110 115 120  
Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln  
125 130 135  
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys  
140 145 150  
Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu  
155 160 165  
Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala  
170 175 180



Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
 185 190 195  
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
 200 205 210  
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly  
 215 220 225  
 Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
 230 235 240  
 Ser Val Ala Asn Ile Met Pro  
 245

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 250  
 aagcttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 251  
 tgacccatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccgggccg gcctggcaag ggggacgagt 50  
cagtggacac tccaggaaga gcgggccccg ggggggcgat gaccgtgcgc 100  
tgacctgac tcaactccagg tccggaggcg gggggccccg gggcgactcg 150  
ggggcggaac gcggggcgga gctgccgccc gtgagtccgg ccgagccacc 200  
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250  
ccgcatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300  
cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350  
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gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800  
cgacccgaat ttcaagtcca ctgccctggt gggtgatggc gagctctaca 850  
ctggaacagt cagcagcttc caagggaatg acccggccat ctcgcgagac 900  
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gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250  
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gaccaccccg gtgccacac cccggcctgg agcgtgcatc accaacagtg 1450

cccgggaaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg 1500  
 aacttctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550  
 gctgctgctg cagccccagg ctgctacca gcgcgtggct gtacaccgag 1600  
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 ggagctgcag atcttctcat cgggacagcc cgtgcagaat ctgctcctgg 1750  
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 gtgcccattg ccaactgcag cctgtaccgg agctgtgggg actgcctcct 1850  
 cgccggggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900  
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 ctgctccagt tcatggcctc ccaggggtgc tggggatgca tccaaagtgg 3150  
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 actctaaggg atatcaacac tgcccagcac aggggccctg aatttatgtg 3700  
 gtttttatac attttttaat aagatgcact ttatgtcatt ttttaataaa 3750  
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253  
 <211> 837  
 <212> PRT  
 <213> Homo sapiens

<400> 253  
 Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro  
 1 5 10 15  
 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu  
 20 25 30  
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser  
 35 40 45  
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu  
 50 55 60  
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu  
 65 70 75  
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80										85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr					
				95					100					105					
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys					
				110					115					120					
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile					
				125					130					135					
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly					
				140					145					150					
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn					
				155					160					165					
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp					
				170					175					180					
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala					
				185					190					195					
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe					
				200					205					210					
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro					
				215					220					225					
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe					
				230					235					240					
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu					
				260					265					270					
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile					
				275					280					285					
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp					
				290					295					300					
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp					
				305					310					315					
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro					
				320					325					330					
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr					
				335					340					345					
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val					
				350					355					360					
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys					
				365					370					375					

Glu Val Asn Arg	Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val	Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val			

665					670					675				
Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	Val	Pro
				680					685					690
Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys
				695					700					705
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
				710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe
				725					730					735
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln
				740					745					750
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu
				755					760					765
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr
				770					775					780
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro
				785					790					795
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile
				800					805					810
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg
				815					820					825
Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val			
				830					835					

<210> 254  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 254  
 agcccgtagca gaatctgctc ctgg 24

<210> 255  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 255  
tgaagccagg gcagcgtcct ctgg 24

<210> 256  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 256  
gtacaggctg cagttggc 18

<210> 257  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 257  
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 258  
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259  
<211> 4563  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 3635  
<223> unknown base

<400> 259  
ctaagccgga ggatgtgcag ctgcggcggc ggcgccggct acgaagagga 50  
cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100  
agggcgggac gggagcccg gactcgtctgc cgccgccgtc gtcgccgtcg 150



tgcgcggccccc	gcgtcccccgc	gcgcgagcgcg	gaggagccgc	cgccacctcg	200
cgcccgagcc	gccgctagcg	cgcgccggggc	atggtcccct	cttaaaggcg	250
caggccgcgg	cggcggggggc	gggtgtgcgg	aacaaagcgc	cggcgcgggg	300
cctgcggggcg	gctcggggggc	cgcgatggggc	gcggcggggcc	cgcggcggcg	350
gcggcgctgc	ccgggcccggg	cctcgcgggcg	ctagggcgggg	ctggccctccg	400
tgggcgggggg	cagcggggctg	agggcgcgcg	gagcctgcgg	cggcggcggc	450
ggcggcggcg	gcggccccggc	gggcggagcg	gcgcgggcat	ggccgcgcgc	500
ggccggcgcg	cctgggtcag	cgtgctgctc	gggtcgtcc	tgggcttcgt	550
gctggcctcg	cggtcgtcc	tgccccgggc	ttccgagctg	aagcgagcgg	600
gcccacggcg	ccgcgccagc	cccgagggct	gccgggtccgg	gcaggcgggcg	650
gcttcccagg	ccggcgggggc	gcgcggcgat	gcgcgcgggg	cgcagctctg	700
gcgcgccggc	tgggacccag	atggcgggccc	gcgcgacagg	aactttctct	750
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gaagaaatgg	gaaaactggc	cctggagcct	ggtgagaact	tctgcatggg	1150
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ccgcaagata	tccgagctcc	gccatcgcac	aatacagctg	caccgcgaaa	1500
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ggagattctg gaatgggagt ttctgactgg aaaatacttg tattcggcag 1650  
 ttgacggcca gccccctcga agaggaatgg actccgcca gagggagcc 1700  
 ttggacgaca ttgtcatgca ggtcatggag atgatcaatg ccaacgcca 1750  
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 ggggtgaacc catgtatggg gctgagtaca tcctggacct gctgcttctg 1850  
 taaaaaagc acaaagggaa gaaaatgacg gtccctgtga ggaggcacgc 1900  
 gtatttacag cagactttca gcaaaatcca gtttgtggag catgaggagc 1950  
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 tcctttctct caaactccct gaagaagctc gtccccttcc agtcccctgg 2050  
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 gagaagacgt gtcttatccc caatcagaac gtcaagctcg tggttctgct 2200  
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 ccagctttgc tggaaaagac gtttttaatt atctaattta tttttcaaaa 2950  
 attttttgta tgatcagttt ttgaagtccg tatacaagga tatattttac 3000  
 aagtggtttt cttacatagg actcctttaa gattgagctt tctgaacaag 3050

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 agcagacctg ctttaactttg acttgaaatg tacctgatga acaaaacttt 3150  
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 ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500

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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly  
1 5 10 15

Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg  
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro  
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly  
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser  
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly  
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala  
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe  
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro  
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe  
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu  
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg  
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe  
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu  
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val  
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly  
230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530					535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu
				545					550					555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu
				560					565					570
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu
				575					580					585
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln
				590					595					600
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu
				605					610					615
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys
				620					625					630
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg
				635					640					645
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
				650					655					660
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
				665					670					675
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
				680					685					690
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
				785					790					795
Asn	Gly	Ser	Val	Arg	Thr	Ala								
				800										

<210> 261  
<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 261  
gtgccactac ggggtgtgga cgac 24

<210> 262  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 262  
tcccatttct tccgtggtgc ccag 24

<210> 263  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 263  
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
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tgacaccttc cctttcggcc ttgaggttcc cagcctggtg gcccaggac 100  
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250  
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300  
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350  
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500  
 tggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550  
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600  
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650  
 ccatatgtta cctcatataa gtcacctgtc accactttag ataagagcac 700  
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcagggtg 750  
 aaactgcatg agaaaaaccc gaagagtttg gaaagcacc agagagtttg 800  
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 acaggcactt cttagtgcac ccagcaaccc agcatataga gaagatattg 900  
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950  
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000  
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050  
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 aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250  
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300  
 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350  
 atgtgttatg aacaattttc atatgcacta aaaaccta ataaaaataaa 1400  
 attttggttc aggaaaaaa 1419

<210> 265  
 <211> 350  
 <212> PRT  
 <213> Homo sapiens

<400> 265  
 Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser  
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 Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu  
 20 25 30  
 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg  
 35 40 45  
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser



					50					55					60	
Pro	Lys	His	Val	Tyr	65	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys	75
Glu	Leu	Val	Thr	His	80	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu	90
Thr	Asn	Pro	Ile	Ser	95	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly	105
Phe	Thr	Pro	Glu	Ile	110	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro	120
Phe	Trp	Ser	Ile	Lys	125	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala	135
Glu	Glu	Pro	Tyr	Ile	140	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	150
Pro	Ala	Ala	Lys	Gln	155	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val	165
Thr	Glu	Ser	Ser	Thr	170	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro	180
Val	Thr	Thr	Leu	Asp	185	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu	195
Ser	Glu	Asp	Val	Pro	200	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys	210
Pro	Glu	Glu	Phe	Gly	215	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp	225
Ile	Leu	Lys	Lys	Ile	230	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala	240
Leu	Leu	Ser	Asp	Thr	245	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu	255
Ala	Ser	Lys	Asp	His	260	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala	270
Ala	Glu	His	Lys	Leu	275	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro	285
Val	Gly	Arg	Thr	Ser	290	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile	300
Asn	Met	Leu	Cys	Asn	305	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp	315
Ile	Lys	Cys	Val	Pro	320	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val	330
Phe	Asn	Thr	Leu	Lys	335	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala	345



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cacaacctcc caggctctc atttgctagt cacggacagt gattcctgcc 1900  
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcaggtt 1950  
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aatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100  
ataaagagga ggtaggattt ttactgatt ctataagccc agcattacct 2150  
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200  
gtccatatcc ctcatthaaca cagacacaaa aattctaaat aaaattttta 2250  
caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300  
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aaa 2403

<210> 267  
<211> 466  
<212> PRT  
<213> Homo sapiens

<400> 267  
Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val  
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

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Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu	35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe	50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser	65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp	80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr	95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile	110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly	125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile	140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg	170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile	185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu	200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu	215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu	230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile	245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys	290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro	305	310	315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val  
320 325 330  
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val  
335 340 345  
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp  
350 355 360  
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn  
365 370 375  
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr  
380 385 390  
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr  
395 400 405  
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe  
410 415 420  
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys  
425 430 435  
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr  
440 445 450  
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp  
455 460 465

Gly

<210> 268  
<211> 2103  
<212> DNA  
<213> Homo sapiens

<400> 268  
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gtcatcttca tatccctgat tgccttgga gtgtgcattg gactcactgt 150  
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350  
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agatttcact ctactgagga tcttgaaact gtagataaaa ttgttcaact 450  
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

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 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600  
 caggatcggt ggtgggacag aagtagaaga ggggtgaatgg ccctggcagg 650  
 ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700  
 gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750  
 tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800  
 aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850  
 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900  
 aatgcagta catagagttt gtctccctga tgcctcctat gagtttcaac 950  
 caggatgatg gatgtttgtg acaggatttg gagcactgaa aatgatggt 1000  
 tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050  
 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100  
 tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggtgactct 1150  
 ggaggaccac tgggttagttc agatgctaga gatatctggt accttgctgg 1200  
 aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctggtgttt 1250  
 atactagagt tacggccttg cgggactgga ttacttcaaa aactggtatc 1300  
 taagagacaa aagcctcatg gaacagataa catttttttt tgttttttgg 1350  
 gtgtggaggc cattttttaga gatacagaat tggagaagac ttgcaaaaca 1400  
 gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450  
 ttcccagctc tggtccgcac gtaagcatcc tgcttctgcc agatcaactc 1500  
 tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550  
 atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600  
 cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650  
 agcaactcct ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700  
 attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750  
 tcccctacat ttatttgga cagaaaagta ttaggtgttt ttcttagtgg 1800  
 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850  
 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900  
 tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

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atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatattat 2050
ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
cca 2103
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<210> 269
<211> 423
<212> PRT
<213> Homo sapiens
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<400> 269														
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Trp	Glu	Pro	Trp	Val 20	Ile	Gly	Leu	Val	Ile 25	Phe	Ile	Ser	Leu	Ile 30
Val	Leu	Ala	Val	Cys 35	Ile	Gly	Leu	Thr	Val 40	His	Tyr	Val	Arg	Tyr 45
Asn	Gln	Lys	Lys	Thr 50	Tyr	Asn	Tyr	Tyr	Ser 55	Thr	Leu	Ser	Phe	Thr 60
Thr	Asp	Lys	Leu	Tyr 65	Ala	Glu	Phe	Gly	Arg 70	Glu	Ala	Ser	Asn	Asn 75
Phe	Thr	Glu	Met	Ser 80	Gln	Arg	Leu	Glu	Ser 85	Met	Val	Lys	Asn	Ala 90
Phe	Tyr	Lys	Ser	Pro 95	Leu	Arg	Glu	Glu	Phe 100	Val	Lys	Ser	Gln	Val 105
Ile	Lys	Phe	Ser	Gln 110	Gln	Lys	His	Gly	Val 115	Leu	Ala	His	Met	Leu 120
Leu	Ile	Cys	Arg	Phe 125	His	Ser	Thr	Glu	Asp 130	Pro	Glu	Thr	Val	Asp 135
Lys	Ile	Val	Gln	Leu 140	Val	Leu	His	Glu	Lys 145	Leu	Gln	Asp	Ala	Val 150
Gly	Pro	Pro	Lys	Val 155	Asp	Pro	His	Ser	Val 160	Lys	Ile	Lys	Lys	Ile 165
Asn	Lys	Thr	Glu	Thr 170	Asp	Ser	Tyr	Leu	Asn 175	His	Cys	Cys	Gly	Thr 180
Arg	Arg	Ser	Lys	Thr 185	Leu	Gly	Gln	Ser	Leu 190	Arg	Ile	Val	Gly	Gly 195
Thr	Glu	Val	Glu	Glu 200	Gly	Glu	Trp	Pro	Trp 205	Gln	Ala	Ser	Leu	Gln 210
Trp	Asp	Gly	Ser	His 215	Arg	Cys	Gly	Ala	Thr 220	Leu	Ile	Asn	Ala	Thr 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro  
 230 235 240

Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys  
 245 250 255

Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys  
 260 265 270

His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser  
 275 280 285

Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp  
 290 295 300

Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly  
 305 310 315

Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg  
 320 325 330

Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro  
 335 340 345

Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly  
 350 355 360

Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly  
 365 370 375

Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly  
 380 385 390

Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly  
 395 400 405

Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys  
 410 415 420

Thr Gly Ile

<210> 270  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

<400> 270  
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 aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100  
 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccaactgtctc 150  
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200  
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250



gatgagactg	agacggcgtg	gccgcctttg	ccggctgtcc	cctgcgacta	300
cgaccactgc	cgacacctgc	aggtgccctg	caaggagcta	cagagggtcg	350
ggccggcggc	ctgcctgtgc	ccaggactct	ccagccccgc	ccagccgccc	400
gacccgccgc	gcatgggaga	agtgcgcatt	gcggccgaag	agggccgcgc	450
agtggccac	tggtgtgccc	ccttctcccc	ggtcctccac	tactggctgc	500
tgctttggga	cggcagcgag	gctgcgcaga	aggggcccc	gctgaacgct	550
acggtccgca	gagccgaact	gaaggggctg	aagccagggg	gcattttatgt	600
cgtttgcgta	gtggccgcta	acgaggccgg	ggcaagccgc	gtgccccagg	650
ctggaggaga	gggcctcgag	ggggccgaca	tccttgcttt	cgggccttgc	700
agccgccttg	cggtgccgcc	caacccccgc	actctggtcc	acgcggccgt	750
cggggtgggc	acggccctgg	ccctgctaag	ctgtgccgcc	ctggtgtggc	800
acttctgcct	gcgcgatcgc	tggggctgcc	cgcgccgagc	cgccgcccga	850
gccgcagggg	cgctctgaaa	ggggcctggg	ggcatctcgg	gcacagacag	900
ccccacctgg	ggcgctcagc	ctggcccccg	ggaaagagga	aaacccgctg	950
cctccagggg	gggctggacg	gcgagctggg	agccagcccc	aggctccagg	1000
gccacggcgg	agtcattggt	ctcaggactg	agcgcttggt	taggtccggt	1050
acttggcgct	ttgtttcctg	gctgaggctc	gggaaggaat	agaaaggggc	1100
ccccaatttt	tttttaagcg	gccagataat	aaataatgta	acctttgcgg	1150
ttaaaaaaaa	aaaaaaaaaa	1170			

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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens
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<400> 271
Met  Leu  Gly  Ser  Pro  Cys  Leu  Leu  Trp  Leu  Leu  Ala  Val  Thr  Phe
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Leu  Val  Pro  Arg  Ala  Gln  Pro  Leu  Ala  Pro  Gln  Asp  Phe  Glu  Glu
          20          25          30

Glu  Glu  Ala  Asp  Glu  Thr  Glu  Thr  Ala  Trp  Pro  Pro  Leu  Pro  Ala
          35          40          45

Val  Pro  Cys  Asp  Tyr  Asp  His  Cys  Arg  His  Leu  Gln  Val  Pro  Cys
          50          55          60

Lys  Glu  Leu  Gln  Arg  Val  Gly  Pro  Ala  Ala  Cys  Leu  Cys  Pro  Gly
          65          70          75

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Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu  
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys  
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp  
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val  
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val  
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro  
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe  
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu  
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser  
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly  
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu  
230 235

<210> 272  
<211> 2397  
<212> DNA  
<213> Homo sapiens

<400> 272  
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cccaggcggg cgtggggcac cgggccccagc gccgacgatc gctgccgttt 150  
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200  
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250  
acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300  
tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350  
aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac 400  
cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatggttagga 450  
tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550  
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aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650  
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tactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750  
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cagtgcactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850  
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900  
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950  
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000  
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050  
agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100  
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150  
caacttggtt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200  
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250  
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300  
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350  
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400  
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450  
atgggtgggac tggagccata gtaaagggtg atttacttct accaactagt 1500  
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550  
acttttatta ctgagcgatc tattcttctg atgctaaata aattatatat 1600  
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650  
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agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000  
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 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200  
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<210> 273  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 273  
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 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu  
 35 40 45  
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe  
 50 55 60  
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile  
 65 70 75  
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu  
 80 85 90  
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys  
 95 100 105  
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met  
 110 115 120  
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met  
 125 130 135  
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp  
 140 145 150  
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe  
 155 160 165  
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys	Ser Lys Gln Ala His Gln	
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys Met	
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg Phe	
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln	Ile Leu Ala Met Ile Leu	
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu Pro	
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys	Asn Asp Asn Ser Gln His	
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser Arg	
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn	Ser Phe Asn Thr His Phe	
290	295	300
Glu Met Glu Glu Leu		
305		

<210> 274  
 <211> 2063  
 <212> DNA  
 <213> Homo sapiens

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Lys	Phe	Glu	Asn	Leu 110	Leu	Asn	Val	Leu	Glu 115	Tyr	Leu	Ala	Leu	Gln 120
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 gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400  
 ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450



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 actgtacctg ttccagcata tcccactat ctctctttct cctgatctgt 2050  
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 cattccttca gacctctccc tgccagtatg ctaaaccctc cctctctctt 2150  
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<210> 287  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 287  
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 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly  
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 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys  
 35 40 45  
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Gly Gly Pro Gly  
 50 55 60  
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala  
 65 70 75  
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn  
 80 85 90  
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu  
 95 100 105  
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val  
 110 115 120  
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn  
 125 130 135  
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val  
 140 145 150  
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala  
 155 160 165  
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser



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<210> 292
<211> 388
<212> PRT
<213> Homo sapiens
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<400> 292

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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	275	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	290	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	305	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	320	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	335	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	350	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	365	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	380	385

<210> 293  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 293  
 gctgacctgg ttcccatcta ctcc 24

<210> 294  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 294  
 cccacagaca cccatgacac ttcc 24

<210> 295  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>



<221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 295  
 aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296  
 <211> 3060  
 <212> DNA  
 <213> Homo sapiens

<400> 296  
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 cggggccgcg gagggcagcg cggggacgcc cgcgcgacga gcaggtggcg 150  
 gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
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 caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
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 tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400  
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 cggaccaggc caggtagag cgctttggga aggagcacgc agtcatcatc 550  
 ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600  
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 accctgtctc 3060

<210> 297  
 <211> 368  
 <212> PRT  
 <213> Homo sapiens

<400> 297  
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 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu  
 35 40 45  
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln  
 50 55 60  
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu  
 65 70 75  
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala  
 80 85 90  
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly  
 95 100 105  
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val  
 110 115 120  
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr  
 125 130 135  
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu  
 140 145 150  
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr  
 155 160 165

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
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Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 298  
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<210> 299  
 <211> 21  
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

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<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100

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tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tcttaggac aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450

tgtcgttctt gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500

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atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600

ctggcctgac agaattctcat cttgttttaat gctctcataa gaccacttgt 650

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 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200  
 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aacctgggag 1250  
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 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 302  
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 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe  
 20 25 30  
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly  
 35 40 45  
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val  
 50 55 60  
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp  
 65 70 75  
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr  
 80 85 90  
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln  
 95 100 105  
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu  
 110 115 120  
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr  
 125 130 135  
 Cys Gly Val Leu Leu Ser Phe Leu

140

<210> 303  
<211> 1768  
<212> DNA  
<213> Homo sapiens

<400> 303  
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tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200  
tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
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gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750  
acaggacttg cattctcctg gaacatgagg gaacgccga ggaaagcaaa 800  
gtggcagga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850  
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ggaagggctg ccgatggcg atgacacact cgggactcac ctctggggcc 950  
atcagacagc cgtttccgcc ccgatccag taccagctgc tgaagggcaa 1000  
ctgcaggccg atgtctctcat cagccaggca gcagccaaaa tctgcgatca 1050  
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ctccctcct tccctctgag aggcctcct atgtccctac taaagccacc 1150  
agcaagacat agctgacagg ggctaattgg tcagtgttgg cccaggaggt 1200  
cagcaaggcc tgagagctga tcagaaggcc ctgctgtgcg aacacggaaa 1250





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<210> 306  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
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 20 25 30  
 Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys  
 35 40 45  
 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser  
 50 55 60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu  
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln  
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys  
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu  
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val  
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala  
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu  
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp  
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr  
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val  
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly  
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg  
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly  
245 250 255

Leu Thr Leu Ala Phe Lys Ile  
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<210> 307  
<211> 2272  
<212> DNA  
<213> Homo sapiens

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gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150  
ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200  
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

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agcgcagagg acaaggagca cgaggagggt cgggactcgg aggagggggc 1950  
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actataaacg gttttttaat ga 2272

<210> 308  
<211> 671  
<212> PRT  
<213> Homo sapiens

<400> 308  
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35 40 45  
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro  
50 55 60  
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys  
65 70 75  
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala  
80 85 90  
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala  
95 100 105  
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp  
110 115 120  
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala  
125 130 135  
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser
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Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala
				170					175					180
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu
				185					190					195
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala
				200					205					210
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys
				215					220					225
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser
				230					235					240
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser
				245					250					255
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val
				260					265					270
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro
				275					280					285
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser
				290					295					300
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu
				305					310					315
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg
				320					325					330
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
				335					340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly
				350					355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg
				365					370					375
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly
				380					385					390
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
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Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser
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Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
				425					430					435

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Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
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    455                                460                                465
Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
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Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
    485                                490                                495
Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
    500                                505                                510
Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
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Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
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Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
    545                                550                                555
Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
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Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
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Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
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Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
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Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
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Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
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Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
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<210> 309
<211> 3871
<212> DNA
<213> Homo sapiens

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<400> 309
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cagcctcaat aattatatta aattaacacc atttgaaaga gaacattgtt 100

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 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200  
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250  
 tacaaagact tgctgctttc aaatagctgt attccctttt tgggttcatac 300  
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350  
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 aacaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450  
 attatgtaaa ttagctggga aagatgccaa tacagaatgt gcaaatttca 500  
 tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550  
 ggagcatttc atccaatatg tgggtatatt gatcttggag tctacaagga 600  
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 aatgtccttt cgatcctcag cagccttttg cttcagtaat gacagatgag 700  
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<210> 310
<211> 777
<212> PRT
<213> Homo sapiens
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<400> 310
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Phe His Leu Phe Pro Ala Leu Met Met Leu Ser Met Thr Met Leu
      20      25      30

Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
      35      40      45

Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
      50      55      60

Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
      65      70      75

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

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80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
				95					100					105					
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
				110					115					120					
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
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Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
				155					160					165					
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
				185					190					195					
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
				215					220					225					
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
				230					235					240					
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
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Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
				275					280					285					
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
				290					295					300					
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
				305					310					315					
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
				320					325					330					
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
				350					355					360					
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
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 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

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Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu				
680	685				690
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu				
695	700				705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu				
710	715				720
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp				
725	730				735
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp				
740	745				750
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His				
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Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr				
770	775				

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 <223> Synthetic construct.  
  
 <400> 311  
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 <213> Artificial  
  
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 <221> Artificial Sequence  
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 <223> Synthetic construct.  
  
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 <212> DNA  
 <213> Artificial  
  
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 <223> Synthetic construct.

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<210> 314  
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<212> DNA  
<213> Homo sapiens

<400> 314  
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 tttcttgtct ttatctaata aactcaatat taag 3934

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 <211> 370  
 <212> PRT  
 <213> Homo sapiens

<400> 315  
 Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr  
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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu	20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala			



305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly		
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro		
335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Pro Ala Lys Ala		
350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
365	370	

<210> 316  
 <211> 4407  
 <212> DNA  
 <213> Homo sapiens

<400> 316  
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<212> PRT  
<213> Homo sapiens

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Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu  
35 40 45  
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu  
50 55 60  
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser  
65 70 75  
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu  
80 85 90  
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu  
95 100 105  
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly  
110 115 120  
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp  
125 130 135  
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro	Leu
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His	Ile
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys	Asn
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg	Ala
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val	Val
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys	Arg
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys	His
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu	Val
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser	Ala
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu	Asn
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile	Leu
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr	Leu
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser	Cys
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala	Ala
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser	Lys
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His	Val
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp	Ser
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly	Tyr
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu	Pro
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln  
440 445 450

Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro  
455 460 465

Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala  
470 475 480

Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys  
485 490 495

Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp  
500 505 510

Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro  
515 520 525

Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val  
530 535 540

Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly  
545 550 555

Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn  
560 565 570

Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu  
575 580 585

Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe  
590 595 600

Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro  
605 610 615

Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr  
620 625 630

Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser  
635 640 645

Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala  
650 655 660

Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys  
665 670 675

Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly  
680 685 690

Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile  
695 700 705

Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro  
710 715 720

Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys	830		835		

<210> 318  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
 ccctgaagct gccagatggc tcc 23

<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctctt cgggtgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321  
<211> 1197  
<212> DNA  
<213> Homo sapiens

<400> 321  
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgtttggta tcctggccct aactctaatt gtctgtttt 200  
gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350  
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650  
actttgagga ggaggagaa gatcttact ttcttgcaa cgaaaaaaaa 700  
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750  
gaccggtcac gccagacaag caagtgagga agaacttcca ataatgact 800  
atactgaaaa tggaatagaa ttgatccca tgctggatga gagaggttat 850  
tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900  
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950  
tcctctgtcg tgcctcatg ccttgtaact ggtgggtggc ccgcatgctg 1000  
gggagggtct aataggaggt ttgagctcaa atgcttaa ac tgctggcaac 1050  
atataataaa tgcctgctat tcaatgaatt tctgcctatg aggcatctgg 1100  
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150  
tgctctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322



<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu  
 1 5 10 15  
 Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys  
 20 25 30  
 Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val  
 35 40 45  
 Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys  
 50 55 60  
 Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys  
 65 70 75  
 Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe  
 80 85 90  
 Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe  
 95 100 105  
 Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys  
 110 115 120  
 Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro  
 125 130 135  
 Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe  
 140 145 150  
 Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn  
 155 160 165  
 Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn  
 170 175 180  
 Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu  
 185 190 195  
 Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala  
 200 205 210  
 Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro  
 215 220 225  
 Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu  
 230 235 240  
 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe  
 245 250 255  
 Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg  
 260 265 270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
 275 280 285  
 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
 290 295 300  
 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
 305 310 315  
 Arg Val

<210> 323  
 <211> 1174  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
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 cagggagctg cccggtcggc ctaggcaggc agccgcacca tggccagcac 100  
 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150  
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200  
 accaacatcc tcacggccgt gtcctacctg aaagggtctt ggatggagtg 250  
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300  
 tggcgtgccc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350  
 tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400  
 cacgcgctgc gccaaaggga caccgcgcaa gaccaccttt gccatcctcg 450  
 gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500  
 tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550  
 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600  
 cgtccctctc gtcattggtt ggcaccctgc tttgcctgtc ctgccaggac 650  
 gaggcaccct acaggcccta ccaggccccg cccaggggcca ccacgaccac 700  
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750  
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800  
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850  
 gtccccggcg ggactgtcaa tggaggcagg ggttcagca caaagtttac 900  
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950  
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
atatttatgt ggggtgatttg ataacaagtt taatataaag tgacttgagg 1100  
gtttggtcag tgggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150  
ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324  
<211> 239  
<212> PRT  
<213> Homo sapiens

<400> 324  
Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe  
1 5 10 15  
Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp  
20 25 30  
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser  
35 40 45  
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly  
50 55 60  
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln  
65 70 75  
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu  
80 85 90  
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr  
95 100 105  
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu  
110 115 120  
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala  
125 130 135  
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro  
140 145 150  
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr  
155 160 165  
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu  
170 175 180  
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln  
185 190 195  
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala  
200 205 210  
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val  
215 220 225



tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
 ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350  
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
 cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450  
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500  
 tcttattaca gcaacaccat tctaggagtt tctgagctc tccactggag 1550  
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 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850  
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcattg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
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 aggttaaaac taattcttta a 2121

<210> 326  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile  
 1 5 10 15  
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp  
 20 25 30  
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln  
 35 40 45  
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe  
 50 55 60  
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met  
 65 70 75  
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe	Ala Leu Lys Cys Ile Arg	
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys	Ala Asn Met Thr Leu Thr	
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly	Leu Cys Ala Ile Ala Gly	
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val	Thr Asn Phe Trp Met Ser	
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly	Gly Met Val Gln Thr Val	
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala	Leu Phe Val Gly Trp Val	
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly	Val Met Met Cys Ile Ala	
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr	Asn Tyr Lys Ala Val Ser	
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala	Tyr Lys Pro Gly Gly Phe	
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn	Thr Lys Asn Lys Lys Ile	
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp	Glu Val Gln Ser Tyr Pro	
245	250	255
Ser Lys His Asp Tyr Val		
260		

<210> 327  
 <211> 2010  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50  
 gtagcagttc cggagtccag ctggctaaaa ctcattcccag aggataatgg 100  
 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150  
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200  
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250  
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300  
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400  
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450  
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500  
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550  
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600  
 tggaccacgg cactggtgct gattgtttga ggagctctgt tctgctgctg 650  
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
 atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750  
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850  
 caaagaaact ttgattttact gttcttaact gcctaattctt aattacagga 900  
 actgtgcata agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattatth tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acatttatat ctacacataga gacatgctta 1150  
 tatgggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgctttttcag ggaaatcatg gataggggtg aagaagggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
 atcctcttct ccagagggt ttttttttct tgtgtattaa attaacatth 1450  
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500  
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtatth 1650  
 gagtacagac tttgaggttt catcaatata aataaaaagag cagaaaaata 1700  
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750  
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggtc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850  
 ttttactaaa atctgtaaaat actgtatttt tctgttttatt ccaaatttga 1900  
 tgaaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
 aatgaatgtg ttctatttgc ttatacatt tatattaata aattgtacat 2000  
 ttttctaatt 2010

<210> 328  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328  
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly  
 1 5 10 15  
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp  
 20 25 30  
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn  
 35 40 45  
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile  
 50 55 60  
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met  
 80 85 90  
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu  
 110 115 120  
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile  
 125 130 135  
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn  
 140 145 150  
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu  
 155 160 165  
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala  
 170 175 180  
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr  
 185 190 195  
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His  
 200 205 210



Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val  
 215 220 225

<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

<400> 329  
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 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150  
 gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
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 cgcctgggtgc tcacctctgg gattgtcttt gtcattctcag gggctctgac 400  
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450  
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500  
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 ctgcacttgc cctcggggg ggtcccaggg cccagccat tacatggccc 600  
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650  
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700  
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750  
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800  
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850  
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900  
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 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050  
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 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150  
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 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgacct 1250

gccccctcg tctcaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA





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tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334  
<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 334  
Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr  
1 5 10 15  
Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30  
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45  
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60  
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75  
Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335  
<211> 742  
<212> DNA  
<213> Homo sapiens

<400> 335  
cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50  
ctgctcgcgc cccgcccgcca tggctgcctc ccccgcgcg cctgctgtcc 100  
tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150  
ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200  
tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250  
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300  
cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350  
agcgaaatth gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400  
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450  
gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500  
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550  
agcgattctc ttcatgtatc tcctaatagcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
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cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
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1 5 10 15  
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20 25 30  
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150  
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200  
gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300  
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350  
 ggggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400  
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450  
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500  
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 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600  
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 cccggccccct cggggctgga aatcggcagc ctgctgctgc ccctgctgct 700  
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 cgactggga gtgggctcct cggggctcgg catctgctgt cgctgcctcg 1100  
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 aaaaaaaaaa 1310

<210> 338  
 <211> 246  
 <212> PRT  
 <213> Homo sapiens

<400> 338  
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe  
 1 5 10 15  
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 20 25 30  
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
 35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp  
50 55 60

Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg  
65 70 75

His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr  
80 85 90

Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu  
95 100 105

Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp  
110 115 120

Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly  
125 130 135

Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly  
140 145 150

Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys  
155 160 165

Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro  
170 175 180

Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile  
185 190 195

Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu  
200 205 210

Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala  
215 220 225

Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala  
230 235 240

Phe Ala Met Tyr Arg Pro  
245

<210> 339  
<211> 849  
<212> DNA  
<213> Homo sapiens

<400> 339  
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caagacccta agaaccatca gccctcagct gcacctctc ccctccaagg 150  
atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200  
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aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
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tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 340  
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1 5 10 15  
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20 25 30  
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
35 40 45  
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
50 55 60  
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
65 70 75  
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
80 85 90  
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
95 100 105  
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
110 115 120  
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
125 130 135  
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

140

145

<210> 341  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 341  
ccctccaagg atgacaaagg cgc 23

<210> 342  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-29  
<223> Synthetic construct.

<400> 342  
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 343  
atctcaggcg gcatcctgtc agcc 24

<210> 344  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 344  
gtggatgcct gcaagaaggt tggg 24

<210> 345  
<211> 45  
<212> DNA  
<213> Artificial

332

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 345  
 agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45  
  
 <210> 346  
 <211> 2575  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 346  
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 caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
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 ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
 ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350  
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Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly
260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His
275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile
290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile
305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg
320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro
335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg
350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr
365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly
380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly
395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln
410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg
425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu
440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala
455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu
470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu
485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His
500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp
515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg
530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 350  
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
 <211> 2524  
 <212> DNA  
 <213> Homo sapiens

<400> 351  
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
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 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135  
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
 140 145 150  
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
 155 160 165  
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
 170 175 180  
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
 185 190 195  
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
 200 205 210  
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
 215 220 225  
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
 230 235 240

Leu Pro Lys

<210> 353  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 353  
 gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg cctcactcc 50  
 cggccaggat ggcatacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggctgc tggggcccgg cgctatcgcg gccatcgtga 350  
 tcgcgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggccc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser  
 1 5 10 15  
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
 20 25 30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
 35 40 45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
 50 55 60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
 65 70 75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
 80 85 90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
 95 100 105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
 110 115 120

Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
 ggccgttggt tggcgcgagg ctgaaggggtg tggcgcgagg agcgctggtg 50  
 gttggccggc ggcgggccgg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactgc cacagcaact 150  
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200  
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccgggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggttat ttccccaacg agctgcgaaa 400  
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500  
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
agtagcccc agaggcgctg ggagtgttgc caccgccctc ccctgaagtt 600  
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650  
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750  
acgtcgctg ctttggctat aactgcgagt agggctcagg catcacacc 800  
acctgtcca gggccctact gtccctgggg tcccaggctc tccttgagg 850  
gggctccccg ccttccacct ggctgtcatc gggtagggcg gggccgtggg 900  
ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctcggcgcag 950  
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000  
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100  
ctagaggggc tcccgaggag gtggaacctc aaccagctc tgcgcaggag 1150  
gcggtgcag tccttttctc cctcaaaggt ctccgacct cagctggagg 1200  
cgggcatctt tcctaaaggg tcccatagg gtctggttcc acccatccc 1250  
aggtctgtgg tcagagcctg ggagggttcc ctacgatgg taggggtgcc 1300  
ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350  
tgaggttaagg ccgccctgac ctggaactca gggggagggg gtaaaggag 1400  
agaggagggg ggctagggg tcctctagat cagtgggggc actgcagggtg 1450  
gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500  
acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600  
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650  
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700  
 cataggacca cacgtcccag ctgggaggag aggcctgggg cccccaggga 1750  
 gggaggcagg ggggtggggga catggagagc tgaggcagcc tcgtctcccc 1800  
 gcagcctggt atgccagcc ttaaggtgtc tggagcccc acacttggcc 1850  
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
 gctgggcctg cccagggca acgtgggggc ggagactcag ctggacagcc 1950  
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100  
 ctgcgggatg tgattaaagt cctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
 125 130 135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140	145	150
Ser Pro Arg Gly Asp Leu Pro		
155		
<210> 357		
<211> 1536		
<212> DNA		
<213> Homo sapiens		
<400> 357		
agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt	50	
cctcttattt ctctcactgt gtgagctggc tgcagaagtt gctgcagaag	100	
ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc	150	
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt	200	
cataggcttc ttccaggatt tagaaatacc agcagtgtcc atactccata	250	
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct	300	
gaggtttctga cacactacaa catcactggg aacaccatct gcctctttcg	350	
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca	400	
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg	450	
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat	500	
tcagattcat ctctcctga taatgaacaa ggcctcccca gagtatgaag	550	
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt	600	
ctctttattc tgggtggacag tggatatgaa gaaaatggga aggtgatatc	650	
atctttcaca ctaaaggagt ctcaactgcc agctttggca atttaccaga	700	
ctctagatga cgagtgggat acactgcca cagcagaagt ttccgtagag	750	
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga	800	
aaatcgtaga tcagaaggaa agactccaaa ggtggaactc tgacttctcc	850	
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac	900	
aactcaaate tcagagacac taaacaacag gatcactagg cctgccaacc	950	
acacacacac gcacgtgcac acacgcacgc acgctgtcac acacacacgc	1000	
gcacacacac acacacacag agcttcattt cctgtottaa aatctcgttt	1050	
tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc	1100	
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga	1150	
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc	1200	



Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 359  
 ccagcagtgccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362



<211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 362  
 attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
 <211> 1777  
 <212> DNA  
 <213> Homo sapiens

<400> 363  
 ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50  
 ccggcgcggg tggcgagag atcagaagcc tcttcccaa gccgagcaa 100  
 cctcagcggg gacccgggct cagggacgcg gcgcggcgcg cggcgactgc 150  
 agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
 cccagacagc cggcgctggc tgtggctcgg gctggcggcg gcgcttgggc 250  
 tcttgacagc tggagtatca gccttggaa tatatacgcc aaaagaaatc 300  
 ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350  
 tagtacgact ggcggttgta cctcagcttc ctggagcttc cagccagagg 400  
 gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
 cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
 tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550  
 atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600  
 cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650  
 tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700  
 ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
 aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
 gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
 tgccttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900  
 tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
 tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100  
ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200  
atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
caattgggag atttcagaaa ctttcctttc accatcattt agaaatgggt 1300  
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
ccttttaatc taagggttta agactgatta gtcttagcat ttactgtagt 1400  
tggaggatgg agatgctatg atggaagcat acccagggtg gccttttagca 1450  
cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccatttgg 1500  
ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700  
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364  
<211> 269  
<212> PRT  
<213> Homo sapiens

<400> 364  
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp  
1 5 10 15  
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
20 25 30  
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
35 40 45  
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
50 55 60  
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
65 70 75  
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
80 85 90  
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile  
110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys  
125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile  
140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val  
155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr  
170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn  
185 190 195

Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser  
200 205 210

Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly  
215 220 225

Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro<sup>8</sup> Val Ile  
230 235 240

Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile  
245 250 255

Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn  
260 265

<210> 365  
<211> 1321  
<212> DNA  
<213> Homo sapiens

<400> 365  
gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50  
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcgggggt 100  
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggcc 150  
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200  
aggggcgcg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgctc 250  
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300  
agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350  
agccgcgacc tgctgcacag gatcaaggat gaggtggggcg caccgggcat 400  
agtggttgga gtttctgtag atggaaaaga agtctgggtca gaaggttttag 450  
gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaaat 950  
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000  
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050  
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaaggt aatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 366  
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro  
 1 5 10 15  
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
 20 25 30  
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
 35 40 45  
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
 50 55 60  
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu  
 65 70 75  
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro  
 80 85 90

[illegible]

<210> 367

<211> 30  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-30  
 <223> Synthetic construct.  
  
 <400> 367  
 tggaaaagaa gtctggtcag aaggtttagg 30  
  
 <210> 368  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 368  
 catttggett cattctcctg ctctg 25  
  
 <210> 369  
 <211> 28  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.  
  
 <400> 369  
 aaaacctcag aacaactcat ttgcacc 28  
  
 <210> 370  
 <211> 41  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-41  
 <223> Synthetic construct.  
  
 <400> 370  
 gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41  
  
 <210> 371  
 <211> 1150  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 371  
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
ctggggcaac ccggtgctc ctgctcttgc tgatggcggt agcagcgccc 150  
agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300  
tcaactgctc ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350  
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
gaagctggtg gctatgtctc ctcttttgc cctgctgtgt ccctggtgga 500  
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600  
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650  
gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700  
agatggaaca ggcccagaag gccaagaacc ccaggagca gaagtccttc 750  
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800  
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000  
tacaagcttg attgaaattc actgctcact tgatacgcta ttcagaaacc 1050  
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe  
50 55 60  
Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu  
65 70 75  
Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu  
80 85 90  
Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn  
95 100 105  
Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp  
110 115 120  
Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys  
125 130 135  
Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val  
140 145 150  
Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro  
155 160 165  
Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu  
170 175 180  
Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly  
185 190 195  
Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala  
200 205 210  
Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys  
215 220 225  
Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser  
230 235 240  
Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly  
245 250 255  
Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu  
260 265

<210> 373  
<211> 1706  
<212> DNA  
<213> Homo sapiens

<400> 373  
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cagcaggtcg tccggggggc caccatgctg gtgaactgcct accttgcttt 150  
tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200



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[illegible]

aaaaaa 1706

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Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
          20          25          30
Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
          35          40          45
Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
          50          55          60
Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
          65          70          75
Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
          80          85          90
Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
          95          100          105
Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
          110          115          120
Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
          125          130          135
Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
          140          145          150
Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
          155          160          165
Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
          170          175          180
Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
          185          190          195
Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
          200          205          210
Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
          215          220          225
Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
          230          235          240

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<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
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Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25						30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40						45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
			50					55						60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
			65					70						75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
			80					85						90



Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val  
 1 5 10 15  
 Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys  
 20 25 30  
 Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly  
 35 40 45  
 Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr  
 50 55 60  
 Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys  
 65 70 75  
 Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile  
 80 85 90  
 His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe  
 95 100 105  
 Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu  
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<210> 379  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 379  
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<210> 380  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 380  
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<210> 381  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45

<223> Synthetic construct.

<400> 381

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<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

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 gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
 ctctctggggg gcccacactg ggcaggggaag atgtatggcc ctggaggagg 200  
 caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
 ggggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300  
 gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
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 ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650  
 ggtatggggc catccgagct gaggccatct gtgtgggtggg ggctgatggg 700  
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 gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

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Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

Gly	Leu	Arg	Val	Ser 50	Val	Gly	Leu	Leu	Leu 55	Val	Lys	Ser	Val	Gln 60
Val	Lys	Leu	Gly	Asp 65	Ser	Trp	Asp	Val	Lys 70	Leu	Gly	Ala	Leu	Gly 75
Gly	Asn	Thr	Gln	Glu 80	Val	Thr	Leu	Gln	Pro 85	Gly	Glu	Tyr	Ile	Thr 90
Lys	Val	Phe	Val	Ala 95	Phe	Gln	Ala	Phe	Leu 100	Arg	Gly	Met	Val	Met 105
Tyr	Thr	Ser	Lys	Asp 110	Arg	Tyr	Phe	Tyr	Phe 115	Gly	Lys	Leu	Asp	Gly 120
Gln	Ile	Ser	Ser	Ala 125	Tyr	Pro	Ser	Gln	Glu 130	Gly	Gln	Val	Leu	Val 135
Gly	Ile	Tyr	Gly	Gln 140	Tyr	Gln	Leu	Leu	Gly 145	Ile	Lys	Ser	Ile	Gly 150
Phe	Glu	Trp	Asn	Tyr 155	Pro	Leu	Glu	Glu	Pro 160	Thr	Thr	Glu	Pro	Pro 165
Val	Asn	Leu	Thr	Tyr 170	Ser	Ala	Asn	Ser	Pro 175	Val	Gly	Arg		

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<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens
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atgtttttcg	ataagaagaa	attgtaggat	ccagtttttt	ttttaaccgc	200	
cccctcccca	cccccaaaa	aaactgtaaa	gatgcaaaaa	cgtaatatcc	250	
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<212> PRT  
<213> Homo sapiens

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Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
35 40 45  
Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
50 55 60  
Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
65 70 75  
Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
80 85 90  
Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
95 100 105  
Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
110 115 120  
Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
125 130 135  
Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
140 145 150  
Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg  
155 160 165  
Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys  
170 175 180  
Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser  
185 190 195  
Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

					200					205					210				
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe					
				215					220					225					
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys					
				230					235					240					
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu					
				245					250					255					
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly					
				260					265					270					
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu					
				275					280					285					
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser					
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Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu					
				305					310					315					
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe					
				320					325					330					
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu					
				335					340					345					
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile					
				350					355					360					
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu					
				365					370					375					
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu					
				380					385					390					
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly					
				395					400					405					
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile					
				410					415					420					
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu					
				425					430					435					
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys					
				440					445					450					
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys					
				455					460					465					
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr					
				470					475					480					
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu					
			</																

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
 500 505 510

Cys Glu Val

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 386  
 ctgggatctg aacagtttcg gggc 24

<210> 387  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 387  
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<210> 388  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-48  
 <223> Synthetic construct.

<400> 388  
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<210> 389  
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 <212> DNA  
 <213> Homo sapiens

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ggatgttgga aaaaattttg gtcattggaga tgttttaaata gtaaagtagc 700  
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
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tctgctttta actctttcct agcatggggc ccataaaaat tattataatt 900  
taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
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tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200  
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcattttattg 1250  
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
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<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5					10					15

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp  
20 25 30  
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln  
35 40 45  
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu  
50 55 60  
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys  
65 70 75  
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala  
80 85 90  
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala  
95 100 105  
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro  
110 115 120  
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser  
125 130 135  
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr  
140 145

<210> 391  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 391  
cttttcagtgcacctcagc gatctc 26

<210> 392  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 392  
ccaaaacatg gagcaggaac agg 23

<210> 393  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.

<400> 393  
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<210> 394  
 <211> 2340  
 <212> DNA  
 <213> Homo sapiens

<400> 394  
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 gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
 aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
 tctctttctac tttgggagag agagaaagtc agatgcccct tttaaactcc 250  
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 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600  
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 cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850  
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 aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

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tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350  
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taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900  
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950  
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accctaactt tgggtaattc tagtataaaa caaattatac ttttatttaa 2050  
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<210> 395  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 395  
Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser  
1 5 10 15



Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu  
 20 25 30  
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
 35 40 45  
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
 50 55 60  
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
 65 70 75  
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
 80 85 90  
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
 95 100 105  
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
 110 115 120  
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
 125 130 135  
 Ser Gly Ser Ile Arg  
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<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
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 gggcccagac aaccggcca tgcttccccg ggtgccaatg cgaggtggag 150  
 acctcgggc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
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 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcatc tcacccactg ctttctcccg ctttcgctac ctggagtcgc 400  
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
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 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
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 ggctgctg ctgcccaccat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700  
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 ggccttacac acctgtctct gccagcctg cagaggctcc ctgagctggc 800  
 gccagtggc ttccgtgagc taccgggcct gcaggctctg gacctgtcgg 850  
 gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggcctgagc 900  
 tccctgcagg agctggacct ttccggcacc aacctggtgc cctgcctga 950  
 ggcgctgctc ctccacctcc cggaactgca gagcgtcagc gtgggccagg 1000  
 atgtgcggtg ccggcgccctg gtgcgggagg gcacctaccc ccggaggcct 1050  
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 tgtgccaaaca ccagtgggga gcccgcaggc ctatgtggca gcgtcaccac 1250  
 aggagtgtg ggcctaggag aggccttgga cctgggagcc acacctagga 1300  
 gcaaagtctc acccctttgt ctacgttgct tcccaaacc atgagcagag 1350  
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 cttatccccc aagtgccttc cctcatgcct gggccggcct gacccgcaat 1450  
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 tgggctgagt gtccccttg gcccatggcc cagtcactca ggggcgagtt 1550  
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 cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900  
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 ttccgagcct ctggaagctt agggcacatt ggttcagcc tagccagttt 2000  
 ctcaccctgg gttggggtcc ccagcatcc agactggaaa cctaccatt 2050  
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gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150  
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 aagctgggca tcagtggcca catgggcac aggggctggc cccacagaga 2500  
 cccacaggg cagtgaagctc tgtcttcccc cacctgccta gcccatcatc 2550  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397  
 <211> 353  
 <212> PRT  
 <213> Homo sapiens

<400> 397  
 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln  
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 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr  
 20 25 30  
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser  
 35 40 45  
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr  
 50 55 60  
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu  
 65 70 75  
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp  
 80 85 90  
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser  
 95 100 105  
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu  
 110 115 120  
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp  
 125 130 135  
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala  
 140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser  
155 160 165

His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly  
170 175 180

Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg  
185 190 195

Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu  
200 205 210

Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe  
215 220 225

Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln  
230 235 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly  
245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala  
260 265 270

Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp  
275 280 285

Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu  
290 295 300

His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg  
305 310 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly  
320 325 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser  
335 340 345

Ala Ala Arg Gly Pro Thr Ile Leu  
350

<210> 398  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 398  
ccctgccagc cgagagcttc acc 23

<210> 399  
<211> 23  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagact acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

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ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatatttaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800  
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gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900  
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
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cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050  
tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100  
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ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
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ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402  
<211> 261  
<212> PRT  
<213> Homo sapiens

<400> 402  
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met  
1 5 10 15  
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu  
20 25 30  
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys  
35 40 45  
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu  
50 55 60  
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu  
65 70 75  
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser  
80 85 90

[illegible]

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<210> 403
<211> 28
<212> DNA
<213> Artificial
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<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.
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<400> 403
ctcctgtggt ctccagattt caggccta 28
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```
<210> 404
<211> 26
<212> DNA
<213> Artificial
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```
<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.
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<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
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gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcgat ttacagacac gtagtgatt ctggaggctg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tccccttttg aaatcagtca ttggagggat gatggctggg gttattggcc 450  
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tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatg gggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccattga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aagggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggctg agaatgaccc cttgggtcaat ggtgttcttg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
1 5 10 15



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Thr	Val	Ala	Glu	Leu 35	Ala	Thr	Phe	Pro	Leu 40	Asp	Leu	Thr	Lys	Thr 45
Arg	Leu	Gln	Met	Gln 50	Gly	Glu	Ala	Ala	Leu 55	Ala	Arg	Leu	Gly	Asp 60
Gly	Ala	Arg	Glu	Ser 65	Ala	Pro	Tyr	Arg	Gly 70	Met	Val	Arg	Thr	Ala 75
Leu	Gly	Ile	Ile	Glu 80	Glu	Glu	Gly	Phe	Leu 85	Lys	Leu	Trp	Gln	Gly 90
Val	Thr	Pro	Ala	Ile 95	Tyr	Arg	His	Val	Val 100	Tyr	Ser	Gly	Gly	Arg 105
Met	Val	Thr	Tyr	Glu 110	His	Leu	Arg	Glu	Val 115	Val	Phe	Gly	Lys	Ser 120
Glu	Asp	Glu	His	Tyr 125	Pro	Leu	Trp	Lys	Ser 130	Val	Ile	Gly	Gly	Met 135
Met	Ala	Gly	Val	Ile 140	Gly	Gln	Phe	Leu	Ala 145	Asn	Pro	Thr	Asp	Leu 150
Val	Lys	Val	Gln	Met 155	Gln	Met	Glu	Gly	Lys 160	Arg	Lys	Leu	Glu	Gly 165
Lys	Pro	Leu	Arg	Phe 170	Arg	Gly	Val	His	His 175	Ala	Phe	Ala	Lys	Ile 180
Leu	Ala	Glu	Gly	Gly 185	Ile	Arg	Gly	Leu	Trp 190	Ala	Gly	Trp	Val	Pro 195
Asn	Ile	Gln	Arg	Ala 200	Ala	Leu	Val	Asn	Met 205	Gly	Asp	Leu	Thr	Thr 210
Tyr	Asp	Thr	Val	Lys 215	His	Tyr	Leu	Val	Leu 220	Asn	Thr	Pro	Leu	Glu 225
Asp	Asn	Ile	Met	Thr 230	His	Gly	Leu	Ser	Ser 235	Leu	Cys	Ser	Gly	Leu 240
Val	Ala	Ser	Ile	Leu 245	Gly	Thr	Pro	Ala	Asp 250	Val	Ile	Lys	Ser	Arg 255
Ile	Met	Asn	Gln	Pro 260	Arg	Asp	Lys	Gln	Gly 265	Arg	Gly	Leu	Leu	Tyr 270
Lys	Ser	Ser	Thr	Asp 275	Cys	Leu	Ile	Gln	Ala 280	Val	Gln	Gly	Glu	Gly 285
Phe	Met	Ser	Leu	Tyr 290	Lys	Gly	Phe	Leu	Pro 295	Ser	Trp	Leu	Arg	Met 300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
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<210> 407  
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<222> 1-31  
<223> Synthetic construct.

<400> 407  
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<220>  
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<222> 1-34  
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gcggaattct taaaatggac tgactccact catc 34

<210> 409  
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<212> DNA  
<213> Homo sapiens

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cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150  
tagataattt tcgttgccca gaatgtgaat gtattgactg gaggtagaga 200  
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250  
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300  
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350  
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ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450  
tgatgttttg gtcacttatt gcttccatgt ggattctttt tggtagatat 500  
gttaccctaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650  
tctgtttgta gatagggttt ttatctctca gtacacattg ccaaattggag 700  
tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750  
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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
1				5					10					15
Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu  
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu  
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala  
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe  
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe  
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr  
155

<210> 411  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-20  
<223> Synthetic construct.

<400> 411  
gtttgaggaa gctgggatac 20

<210> 412  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
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<223> Synthetic construct.

<400> 412  
ccaaactcga gcacctgttc 20

<210> 413  
<211> 40  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-40  
<223> Synthetic construct.

<400> 413  
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<210> 414

<211> 1337  
<212> DNA  
<213> Homo sapiens

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gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctggggccc 100  
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
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aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
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gacttgggga gttcctacgc aaaacaactg ggcttcggg acagctgggt 850  
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taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950  
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gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300  
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
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 1 5 10 15  
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
 20 25 30  
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
 35 40 45  
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
 50 55 60  
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
 65 70 75  
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
 80 85 90  
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
 95 100 105  
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
 110 115 120  
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
 125 130 135  
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
 140 145 150  
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
 155 160 165  
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
 170 175 180  
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
 185 190 195  
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
 200 205 210  
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
 215 220

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-21  
 <223> Synthetic construct.  
  
 <400> 416  
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 <210> 417  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 417  
 ggatggccag agctgctg 18  
  
 <210> 418  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 418  
 aaagtacaag tgtggcctca tcaagc 26  
  
 <210> 419  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 419  
 tctgactcct aagtcaggca ggag 24  
  
 <210> 420  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 420  
 attctctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
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<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
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cacgccagga gctcgtctgc tctctctctc tctctctcac tctcctctcc 200  
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gcacccttct ctgggacact atgttgttct ccgccctcct gctggagggtg 300  
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tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850



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tttcctaga tatactgcgg gatctctcct taggataaag agttgctggt 1650  
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700  
t 1701

<210> 423  
<211> 337  
<212> PRT  
<213> Homo sapiens

<400> 423  
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
1 5 10 15  
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
20 25 30  
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
35 40 45  
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
50 55 60  
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
65 70 75  
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80										85					90				
Pro	Ser	Thr	Leu	Tyr 95	Leu	Gly	Gly	Leu		Pro	Arg	Lys	Tyr	Val	Ala 105				
Ala	Gln	Leu	His	Leu 110	His	Trp	Gly	Gln		Lys	Gly	Ser	Pro	Gly	Gly 120				
Ser	Glu	His	Gln	Ile 125	Asn	Ser	Glu	Ala		Thr	Phe	Ala	Glu	Leu	His 135				
Ile	Val	His	Tyr	Asp 140	Ser	Asp	Ser	Tyr		Asp	Ser	Leu	Ser	Glu	Ala 150				
Ala	Glu	Arg	Pro	Gln 155	Gly	Leu	Ala	Val		Leu	Gly	Ile	Leu	Ile	Glu 165				
Val	Gly	Glu	Thr	Lys 170	Asn	Ile	Ala	Tyr		Glu	His	Ile	Leu	Ser	His 180				
Leu	His	Glu	Val	Arg 185	His	Lys	Asp	Gln		Lys	Thr	Ser	Val	Pro	Pro 195				
Phe	Asn	Leu	Arg	Glu 200	Leu	Leu	Pro	Lys		Gln	Leu	Gly	Gln	Tyr	Phe 210				
Arg	Tyr	Asn	Gly	Ser 215	Leu	Thr	Thr	Pro		Pro	Cys	Tyr	Gln	Ser	Val 225				
Leu	Trp	Thr	Val	Phe 230	Tyr	Arg	Arg	Ser		Gln	Ile	Ser	Met	Glu	Gln 240				
Leu	Glu	Lys	Leu	Gln 245	Gly	Thr	Leu	Phe		Ser	Thr	Glu	Glu	Glu	Pro 255				
Ser	Lys	Leu	Leu	Val 260	Gln	Asn	Tyr	Arg		Ala	Leu	Gln	Pro	Leu	Asn 270				
Gln	Arg	Met	Val	Phe 275	Ala	Ser	Phe	Ile		Gln	Ala	Gly	Ser	Ser	Tyr 285				
Thr	Thr	Gly	Glu	Met 290	Leu	Ser	Leu	Gly		Val	Gly	Ile	Leu	Val	Gly 300				
Cys	Leu	Cys	Leu	Leu 305	Leu	Ala	Val	Tyr		Phe	Ile	Ala	Arg	Lys	Ile 315				
Arg	Lys	Lys	Arg	Leu 320	Glu	Asn	Arg	Lys		Ser	Val	Val	Phe	Thr	Ser 330				
Ala	Gln	Ala	Thr	Thr 335	Glu	Ala													

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<210> 424
<211> 18
<212> DNA
<213> Artificial
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<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
    gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
    cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
    ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
    cagaaaccca tgatacccta ctgaacaccg aatccccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
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    gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

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accattaaca	cagatgctca	cactggggcc	agatctgcat	ctgttaaadc	300
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<210> 429
<211> 209
<212> PRT
<213> Homo sapiens
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<400> 429
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Ser  Leu  Pro  Gln  Leu  Lys  Pro  Ala  Leu  Gly  Leu  Pro  Pro  Thr  Lys
      20      25      30

Leu  Ala  Pro  Asp  Gln  Gly  Thr  Leu  Pro  Asn  Gln  Gln  Gln  Ser  Asn
      35      40      45

Gln  Val  Phe  Pro  Ser  Leu  Ser  Leu  Ile  Pro  Leu  Thr  Gln  Met  Leu
      50      55      60

Thr  Leu  Gly  Pro  Asp  Leu  His  Leu  Leu  Asn  Pro  Ala  Ala  Gly  Met
      65      70      75

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Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn  
 80 85 90  
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr  
 95 100 105  
 Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro  
 110 115 120  
 Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly  
 125 130 135  
 Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp  
 140 145 150  
 Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln  
 155 160 165  
 Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp  
 170 175 180  
 Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His  
 185 190 195  
 Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln  
 200 205

<210> 430  
 <211> 1257  
 <212> DNA  
 <213> Homo Sapien

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 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150  
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 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
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 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600  
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Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
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Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
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